

QY 3 GYKSKF 9
Db 1 GIGNNAP 7

RESULT 20

GRAR_RANRU STANDARD; PRT; 12 AA.
ID GRAR_RANRU
AC P40754;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Granuliberin-R.
OS Rana rugosa (Wrinkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP TISSUE=Skin secretion;
RC MEDLINE=78062810; PubMed=589733;
RA Nakajima T., Yasuhara T.;
RT "A new mast cell degranulating peptide, granuliberin-R, in the frog
RT (Rana rugosa) skin.";
RL Chem. Pharm. Bull. 25:2464-2465 (1977).
RN [2]
RP SYNTHESIS.
RX MEDLINE=78189201; PubMed=657408;
RA Nakajima T., Yasuhara T., Hirai Y., Kitada C., Fujino M., Takeyama M.,
RA Koyama K., Yajima H.;
RT "Synthesis of the dodecapeptide amide corresponding to the entire
RT amino acid sequence of granuliberin-R, a new frog skin peptide from
RT Rana rugosa.";
RL Chem. Pharm. Bull. 26:1222-1230 (1978).
CC -1- FUNCTION: Mast cell degranulating peptide.
CC -1- SUBCELLULAR LOCATION: Secreted.
KW Amphibian defense peptide; Mast cell degranulation; Amidation.
FT MOD_RES 12
SQ SEQUENCE 12 AA; 1424 MW; 2B974EB9CAlB5047 CRC64;

Query Match 29.4%; Score 15; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 5.5e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FGY 4
Db 1 FGF 3

RESULT 21

NPL_LYMST STANDARD; PRT; 13 AA.
ID NPL_LYMST
AC P80178;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Lymnaea-Df-amide 1.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93238777; PubMed=8477756;
RA Johnsen A.H., Rehfeld J.F.;
RT "LymnadFamides, a new family of neuropeptides from the pond snail,
RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates?";
RL Eur. J. Biochem. 213:875-879 (1993).
CC -1- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.

DR PIR; S32471; S32471.
KW Neuropeptide; Amidation.
FT MOD_RES 13
SQ SEQUENCE 13 AA; 1519 MW; 9CA07BA3F5D5B455 CRC64;

Query Match 29.4%; Score 15; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 NSKF 9
Db 7 NSAF 10

RESULT 22

NP4_LYMST STANDARD; PRT; 13 AA.
ID NP4_LYMST
AC P80181;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Lymna-Df-amide 4.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93238777; PubMed=8477756;
RA Johnsen A.H., Rehfeld J.F.;
RT "LymnadFamides, a new family of neuropeptides from the pond snail,
RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates?";
RL Eur. J. Biochem. 213:875-879 (1993).
CC -1- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.
DR PIR; S32474; S32474.
KW Neuropeptide; Amidation.
FT MOD_RES 13
SQ SEQUENCE 13 AA; 1503 MW; 9CA07BBB56D55455 CRC64;

Query Match 29.4%; Score 15; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 NSKF 9
Db 7 NSAF 10

RESULT 23

TEML_RANTE STANDARD; PRT; 13 AA.
ID TEML_RANTE
AC P57104;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Temporin U.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;
RA Stimaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria.";
RL Eur. J. Biochem. 242:788-792 (1996).
CC -1- FUNCTION: Has antibacterial activity against Gram-negative and
Gram-positive bacteria.

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CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: Belongs to the brevian family.
KM Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 13 13
SQ SEQUENCE 13 AA; 1641 MW; 98BDB1FAFF7C325 CRC64;

Query Match
Best Local Similarity 29.4%; Score 15; DB 1; Length 13;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SKP 9
DB 6 SKP 8

RESULT 24
MY14_EISFO STANDARD; PRT; 14 AA.
AC P46979;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Myosin-like tetradecapeptide (ETP).
OS Eiseia foetida (Common brandling worm) (Common dung-worm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbricina; Lumbricidae; Eiseia.
OX NCBI_TaxID=6396;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=gut;
RX MEDLINE=96087873; PubMed=8532604;
RA Ukena K., Onmi T., Matsushima O., Ikeda T., Fujita T., Minakata H.,
RA Nomoto K.;
RT "A novel gut tetradecapeptide isolated from the earthworm, Eiseia
RT foetida.";
RL Peptides 16:995-999 (1995).
CC -1- FUNCTION: Has a stimulative effect on the contraction of gut
CC muscles.
CC -1- SIMILARITY: TO INSECTS ALATOTROPIN.
KM Neuropetide; Amidation.
FT MOD_RES 14 14
SQ SEQUENCE 14 AA; 1478 MW; CC9ABEF941CD91AD CRC64;

Query Match
Best Local Similarity 29.4%; Score 15; DB 1; Length 14;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYKN 6
DB 1 GFKD 4

RESULT 25
RS19_PFWBP STANDARD; PRT; 14 AA.
ID RS19_PFWBP
AC Q52093;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S19 (Fragment).
GN P85S OR RPS19.
OS Pigeon pea witches'-broom phytoplasma.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Phytoplasma.
OX NCBI_TaxID=37700;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94350802; PubMed=8071198;
RA Gundersen D.B., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for
RT their classification.";
RL J. Bacteriol. 176:5244-5254 (1994);

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CC -1- FUNCTION: Protein S19 forms a complex with S13 that binds strongly
CC to the 16S ribosomal RNA (By similarity).
CC -1- SIMILARITY: Belongs to the S19 family of ribosomal proteins.
CC -----
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb.ch).
CC -----
DR EMBL; L27036; AAA83946.1; -
DR HAMAP; MF 00531; -; 1.
DR InterPro; IPR002222; Ribosomal_S19.
DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KM Ribosomal protein; rRNA-binding.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1668 MW; 8FD46FB830DFBBA CRC64;

Query Match
Best Local Similarity 29.4%; Score 15; DB 1; Length 14;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 KNSK 8
DB 6 KDSK 9

RESULT 26
SMS1_MYOSC STANDARD; PRT; 14 AA.
ID SMS1_MYOSC
AC P20750;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Somatostatin I.
OS Myoxocephalus scorpius (Shorthorn sculpin) (Daddy sculpin),
OS Oncorhynchus kisutch (Coho salmon), and
OS Anguilla anguilla (European freshwater eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percomorphi; Scorpaeniformes;
OC Corioidi; Cortidae; Myoxocephalus.
OX NCBI_TaxID=8097, 8019, 7936;
RN [1]
RP SEQUENCE.
RC SPECIES=M. scorpius; TISSUE=Pancreas;
RX MEDLINE=88029486; PubMed=2889597;
RA Conlon J.M., Davis M.S., Falkner S., Thim L.;
RT "Structural characterization of peptides derived from
RT prosomatostatins I and II isolated from the pancreatic islets of two
RT species of teleostean fish: the daddy sculpin and the flounder.";
RL Eur. J. Biochem. 168:1647-1652 (1987).
RN [2]
RP SEQUENCE.
RC SPECIES=O. kisutch; TISSUE=Pancreas;
RX MEDLINE=87055212; PubMed=2877919;
RA Plietskaya E.M., Pollock H.G., Rouse J.B., Hamilton J.W.,
RA Kimmel J.R., Andrews P.C., Gorman A.;
RT "Characterization of coho salmon (Oncorhynchus kisutch) islet
RT somatostatins.";
RL Gen. Comp. Endocrinol. 63:252-263 (1986).
RN [3]
RP SEQUENCE.
RC SPECIES=A. anguilla; TISSUE=Pancreas;
RX MEDLINE=89065329; PubMed=2904391;
RA Conlon J.M., Deacon C.F., Hazen N., Henderson I.W., Thim L.;
RT "Somatostatin-related and glucagon-related peptides with unusual
RT structural features from the European eel (Anguilla anguilla).";
RL Gen. Comp. Endocrinol. 72:181-189 (1988).
CC -1- FUNCTION: Somatostatin inhibits the release of somatotropin.
CC -1- SUBCELLULAR LOCATION: Secreted.

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CC -1- SIMILARITY: Belongs to the somatostatin family.
DR PIR; A60840; A60840.
DR PIR; B60842; B60842.
DR PIR; S00172; S00172.
DR InterPro: IPR004250; Somatostatin.
DR Pfam: PF03002; Somatostatin.1.
KW Hormone; Multigene family.
FT DISULFID 3
SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;

Query Match
Best Local Similarity 29.4%; Score 15; DB 1; Length 14;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GYKN 6
DB 2 GCKN 5

RESULT 27
SMS_ALIMI
ID SMS_ALIMI STANDARD; PRT; 14 AA.
AC P31885;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Somatostatin-14.
OS Alligator mississippiensis (American alligator), and
OS Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodyliidae; Alligatorinae; Alligator.
OX NCBI_TaxID=8496, 34903;
RN [1]
RP SEQUENCE.
RC SPECIES=A.mississippiensis; TISSUE=Stomach;
RX MEDLINE=93324451; PubMed=8101369;
RA Wang Y., Conlon J.M.;
RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain
RT and stomach of the alligator.";
RL Peptides 14:573-579(1993).
RN [2]
RP SEQUENCE.
RC SPECIES=T.scripta;
RX MEDLINE=90341082; PubMed=1974347;
RA Conlon J.M., Hicks J.W.;
RT "Isolation and structural characterization of insulin, glucagon and
RT somatostatin from the turtle, Pseudemys scripta.";
RL Peptides 11:461-466(1990).
CC -1- FUNCTION: Somatostatin inhibits the release of somatotropin.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the somatostatin family.
DR PIR; C60414; C60414.
DR InterPro: IPR004250; Somatostatin.
DR Pfam: PF03002; Somatostatin.1.
KW Hormone.
FT DISULFID 3
SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;

Query Match
Best Local Similarity 29.4%; Score 15; DB 1; Length 14;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GYKN 6
DB 2 GCKN 5

RESULT 28
LCKS_LEUMA
ID LCKS_LEUMA STANDARD; PRT; 8 AA.
AC P19887;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)

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DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Leucokinin V (L-V).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberidae;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RX MEDLINE=87052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
RT myotropic peptides of Leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:27-30(1987).
CC -1- FUNCTION: This cephalomyotropic peptide stimulates contractile
CC activity of cockroach prothodum (hindgut).
CC -1- SUBCELLULAR LOCATION: Secreted.
DR PIR; J50315; J50315.
KW Neuropeptide; Amidation.
FT MOD RES 8
SQ SEQUENCE 8 AA; 784 MW; 736365A5B9C86588 CRC64;

Query Match
Best Local Similarity 27.5%; Score 14; DB 1; Length 8;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKN 6
DB 1 GSGFSS 6

RESULT 29
SAMP_MUSCA
ID SAMP_MUSCA STANDARD; PRT; 9 AA.
AC P19095;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serum amyloid P-component (SAP) (Fragment).
OS Mus musculus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphi; Galeoidea; Carchariniformes; Triakidae;
OC Mustelus.
OX NCBI_TaxID=7812;
RN [1]
RP SEQUENCE.
RX MEDLINE=83160932; PubMed=6403520;
RA Rodey F.A., Tanaka T., Liu T.-Y.;
RT "Isolation and characterization of two major serum proteins from the
RT dogfish, Mustelus canis, C-reactive protein and amyloid P
RT component.";
RL J. Biol. Chem. 258:3889-3894(1983).
CC -1- SUBUNIT: Homopentamer. Pentaxin (or pentaxin) have a discoid
CC arrangement of 5 noncovalently bound subunits.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.
CC -1- SIMILARITY: Belongs to the pentaxin family.
DR PIR; B20569; B20569.
DR InterPro: IPR001759; Pentaxin.
DR PROSITE; PS00289; PENTAXIN; PARTIAL.
KW Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.
FT DOMAIN 1
FT NON TER 9
SQ SEQUENCE 9 AA; 965 MW; D05B5735B3386769 CRC64;

Query Match
Best Local Similarity 27.5%; Score 14; DB 1; Length 9;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GFGYKN 9
DB 1 GSGFSS 9

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CC -----
DR EMBL; M74771; AAA21914.1; -.
DR PIR; F41839; F41839.
DR InterPro; IPR000114; Ribosomal_L16.
DR PROSITE; PS00586; RIBOSOMAL_L16_1; PARTIAL.
DR PROSITE; PS00701; RIBOSOMAL_L16_2; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER 10
FT SEQUENCE 10 AA; 1324 MW; B3386A21B4032766 CRC64;
SQ
Query Match 27.5%; Score 14; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 7e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 5 KNSKP 9
|:|:
Db 5 KRTKY 9
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RESULT 32
BFG_CLOPA
ID BFG_CLOPA STANDARD; PRT; 11 AA.
AC P81350;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G (EF-G) (CP 5) (Fragment).
GN RUSA.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OC NCBI_TaxID=1501;
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flensburg R.; Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -1- FUNCTION: This protein promotes the GTP-dependent translocation of
CC the nascent protein chain from the A-site to the P-site of the
CC ribosome.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC EF-G/EF-2 subfamily.
DR InterPro; IPR000795; EF_Grpbind.
DR PROSITE; PS00301; EFACIDR_GTP; PARTIAL.
KW Elongation factor; Protein biosynthesis; GTP-binding.
FT NON_TER 11
FT SEQUENCE 11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;
SQ
Query Match 27.5%; Score 14; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 YNSKP 9
|:|:
Db 2 YPLEKF 7
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RESULT 33
RS19_CLYEP
ID RS19_CLYEP STANDARD; PRT; 12 AA.
AC Q46450;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S19 (Fragment).
GN RPS5 OR RPS19.

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DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neurotensin (NT).
 GN NTS
 OS *Cavia porcellus* (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
 ON NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Small intestine;
 RX MEDLINE=86248085; PubMed=3087775;
 RA Shaw C., Tim L., Conlon J.M.;
 RT "[Ser7]neurotensin: isolation from guinea pig intestine.";
 RL FEBS Lett. 202:187-192(1986).
 CC -1- FUNCTION: Smooth muscle-contracting peptide.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the neurotensin family.
 DR PIR; A53608; A53608.
 KW Vasodilator; Pyroglutamate carboxylic acid.
 FT MOD_RES 1
 FT SEQUENCE 13 AA; 1680 MW; 4C8314644C4115B3 CRC64;

Query Match
 Best Local Similarity 27.5%; Score 14; DB 1; Length 13;
 Best Local Similarity 66.7%; Pred. No. 9e+03;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YRN 6
 DB 3 YEN 5

RESULT 37
 UC18_MAIZE STANDARD; PRT; 14 AA.
 ID UC18_MAIZE
 AC P80624;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 263)
 DS (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACAD clade; Panicoideae; Andropogoneae; Zea.
 ON NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Perrotet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 6.1, its MW is: 50.3 kDa.
 DR Maize-2DPAGE; P80624; COLEOPTILE.
 DR MaizeDB; 123950;
 FT NON_TER 1
 FT SEQUENCE 14 AA; 1485 MW; 2EF9116472A39458 CRC64;

Query Match
 Best Local Similarity 27.5%; Score 14; DB 1; Length 14;
 Best Local Similarity 50.0%; Pred. No. 9.7e+03;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FGKNS 7
 DB 9 FGHTS 14

RESULT 38
 SAZA_ONCMY

ID SAZA_ONCMY STANDARD; PRT; 13 AA.
 AC P8238;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Salmocidin 2A (Fragment).
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 ON NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE AND FUNCTION.
 RC TISSUE=Serum;
 RA Henry M.A., Secombes C.J.;
 RT "Purification and partial characterization of antibacterial peptides
 RT from rainbow trout, *Oncorhynchus mykiss*.";
 RL Submitted (DEC-1999) to Swiss-Prot
 CC -1- FUNCTION: Antibacterial activity against Gram-negative bacteria.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Plasma serum.
 KW Antibiotic.
 FT NON_TER 13
 FT SEQUENCE 13 AA; 1416 MW; 5FFB792AFC645873 CRC64;

Query Match
 Best Local Similarity 26.5%; Score 13.5; DB 1; Length 13;
 Best Local Similarity 57.1%; Pred. No. 1.1e+04;
 Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 GF--GY 4
 DB 2 GFVLKGY 8

RESULT 39
 SA2B_ONCMY STANDARD; PRT; 13 AA.
 ID SA2B_ONCMY
 AC P82239;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DS Salmocidin 2B (Fragment).
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 ON NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE AND FUNCTION.
 RC TISSUE=Serum;
 RA Henry M.A., Secombes C.J.;
 RT "Purification and partial characterization of antibacterial peptides
 RT from rainbow trout, *Oncorhynchus mykiss*.";
 RL Submitted (DEC-1999) to Swiss-Prot.
 CC -1- FUNCTION: Antibacterial activity against Gram-negative bacteria.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Plasma serum.
 KW Antibiotic.
 FT NON_TER 13
 FT SEQUENCE 13 AA; 1400 MW; 5FFB792AFC645873 CRC64;

Query Match
 Best Local Similarity 26.5%; Score 13.5; DB 1; Length 13;
 Best Local Similarity 57.1%; Pred. No. 1.1e+04;
 Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 GF--GY 4
 DB 2 GFVLKGY 8

RESULT 40
 ALLS_CYDPO STANDARD; PRT; 8 AA.
 ID ALLS_CYDPO

```

AC P82156;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiaastatin 5
OS Cydia pomonella (Coaling moth); Insecta; Pterygota;
OC Eukaryota; Metazoa; Arthropoda; Hexapoda;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricoidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=93054539; PubMed=9392829;
RA Davey H., Johnsen A.H., Maestri J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RT Peptides 16:1301-1309(1997).
CC -1- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation.
FT MOD RES 8
SQ SEQUENCE 8 AA; 898 MW; 922879CAB58640D CRC64;

Query Match 25.5%; Score 13; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GY 4
DB 3 GY 4

RESULT 41
NEF_HV128 STANDARD; PRT; 9 AA.
AC P12481;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF) (Fragment).
GN NEF.
OS Human immunodeficiency virus type 1 (Z-84 isolate) (HIV-1).
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11681;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88281278; PubMed=3395517;
RA Youno J., Joseph S.F., Reitz W.S. Jr., Zagury D., Wong-Staal F.,
RA Gallo R.C.;
RT "Nucleotide sequence analysis of the env gene of a new Zairian
RT isolate of HIV-1.";
RT AIDS Res. Hum. Retroviruses 4:165-173(1988).
CC -1- FUNCTION: NEF has GTPase, GTP-binding and autophosphorylating
CC activities. It seems to down-regulate the CD4(74) antigen.
CC -1- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD
CC ZAIREAN MALE.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J03653; AAA44687.1; -
DR HIV; J03653; NEF53Y1
KW AIDS; Myristate; GTP-binding; Lipoprotein.
FT LIPID 2
FT N-myristoyl glycine (in host) (by
FT similarity).
FT NON TER 9
FT SEQUENCE 9 AA; 967 MW; 319CB325A3733878 CRC64;

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Query Match 25.5%; Score 13; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 GYNSK 8
DB 2 GSKMSK 7

RESULT 42
NEU_CAVPO STANDARD; PRT; 9 AA.
ID NEU_CAVPO
AC P34966;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuromedin U-9 (Nmu-9).
GN NMU.
OS Cavia porcellus (Guinea pig); Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Rodentia; Hystriognathi; Cavidae; Cavia.
OX Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE.
RC TISSUE=Small intestine;
RX MEDLINE=90341105; PubMed=2381877;
RA Murphy R., Turner C.A., Furness J.B., Parker L., Giraud A.;
RT "Isolation and microsequence analysis of a novel form of neuromedin U
RT peptides 11:613-617(1990).";
RT Peptides 11:613-617(1990).
CC -1- FUNCTION: Stimulates uterine smooth muscle contraction and causes
CC selective vasoconstriction.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the Nmu family.
CC InterPro: IPR008199; NMU.
DR Pfam; PF02070; NMU; 1.
DR PROSITE; PS00967; NMU; 1.
KW Amidation; Hormone.
FT MOD RES 9
SQ SEQUENCE 9 AA; 1169 MW; 1ECF177409C729DB CRC64;

Query Match 25.5%; Score 13; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GY 4
DB 1 GY 2

RESULT 43
NSKL_SARBU STANDARD; PRT; 9 AA.
ID NSKL_SARBU
AC P41492;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Neosulfakinin-I (NEB-SK-I).
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7365;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RX MEDLINE=93083101; PubMed=1360367;
RA Fonagy A., Schoofs L., Proost P., van Damme J., de Loof A.;
RT "Isolation and primary structure of two sulfakinin-like peptides from
RT the fleshfly, Neobellieria bullata.";
RT Comp. Biochem. Physiol. 103C:135-142(1992).
CC -1- FUNCTION: Myotropic peptide.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

```

DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; 1.
 KM Neuropeptide; Amidation; Sulfation.
 FT MOD_RES 4 4 SULFATION (POTENTIAL).
 FT MOD_RES 9 9 AMIDATION (POTENTIAL).
 SQ SEQUENCE 9 AA; 1187 MW; 850A0691B865AAA CRC64;

Query Match 25.5%; Score 13; DB 1; Length 9;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 YNSKF 9
 DB 4 YGHWRF 9

RESULT 44
 ESTA_SCHGA STANDARD; PRT; 10 AA.
 AC P81012;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Esterase 52 kDa subunit (EC 3.1.1.1) (Carboxylic-ester hydrolase)
 DE (Fragment).
 OS Schizaphis graminum (Aphid).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
 OC Aphidoidea; Aphididae; Aphidini; Schizaphis.
 OX NCBI_TaxId=13262;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=97468499; PubMed=9327586;
 RA Siegfried B.D., Ono M., Swanson U.J.;
 RT "Purification and characterization of a carboxylesterase associated
 with organophosphate resistance in the greenbug, Schizaphis graminum
 (Homoptera: Aphididae).";
 RL Arch. Insect Biochem. Physiol. 36:229-240(1997).
 CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
 carboxylic anion.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 DR InterPro; IPR002018; CarbesteraseB.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; PARTIAL.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; PARTIAL.
 KM Hydrolyase; Serine esterase.
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1025 MW; 018AB3587865A2C0 CRC64;

Query Match 25.5%; Score 13; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GY 4
 DB 7 GY 8

RESULT 45
 HTF_HELZE STANDARD; PRT; 10 AA.
 AC P15353;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypertrichaloseaemic hormone (Hez-HRH).
 OS Heliothis zea (Corn earworm) (Bollworm).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
 OC Noctuidae; Heliothinae; Helioverpa.
 OX NCBI_TaxId=7113;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Corpora cardiaca;
 RX MEDLINE=88326324; PubMed=3415690;
 RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Bird T.G.,
 RA Tseng C.M., Zhang Y.S., Hayes D.K.;
 RT "Isolation and primary structure of a neuropeptide hormone from
 RT Heliothis zea with hypertrichalosemic and adipokinetic activities.";
 RL Biochem. Biophys. Res. Commun. 155:344-350(1988).
 CC -1- FUNCTION: Hypertrichaloseaemic factors are neuropeptides that
 CC elevate the level of trehalose in the hemolymph (trehalose is the
 CC major carbohydrate in the hemolymph of insects).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
 DR PIR; A31571; A31571.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KM Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1096 MW; 8E70367865A5B9D1 CRC64;

Query Match 25.5%; Score 13; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 1.1e+04;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFG 3
 DB 7 GWF 9

Search completed: August 30, 2004, 10:50:20
 Job time : 3.55068 secs

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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:41:54 ; Search time 2.70608 Seconds
(without alignments)
319.918 Million cell updates/sec

Title: US-09-720-469A-3

Perfect score: 51

Sequence: 1 GFGYKNSKF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1638

Minimum DB seq length: 8

Maximum DB seq length: 14

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	45.1	13	2	PT0331
2	23	45.1	14	2	S36678
3	22	43.1	12	2	PH1454
4	22	43.1	13	2	PH0787
5	21	41.2	8	2	PC4373
6	20	39.2	9	2	UP0073
7	20	39.2	10	2	B33995
8	20	39.2	11	2	PT0211
9	20	39.2	14	2	S38307
10	19	37.3	10	2	B61033
11	19	37.3	14	2	B58502
12	18	35.3	9	2	PC7074
13	18	35.3	10	2	B60527
14	18	35.3	10	2	B60527
15	18	35.3	10	2	S06964
16	18	35.3	10	2	PO0753
17	18	35.3	11	2	A44755
18	18	35.3	12	2	S25547
19	18	35.3	12	2	PT0274
20	18	35.3	13	2	A59387
21	18	35.3	13	2	PS0277
22	18	35.3	14	2	IS1432
23	18	35.3	14	2	A17150
24	17	33.3	11	2	I41138
25	17	33.3	11	2	S66649
26	17	33.3	11	2	PH0939
27	17	33.3	13	2	A61361
28	17	33.3	14	2	PH1597
29	17	33.3	14	2	PC7079

30	17	33.3	14	2	C59137	protein pf3 - gold
31	16	31.4	9	2	A42266	peptidylglycine mo
32	16	31.4	10	2	C45474	thrombospondin 2 -
33	16	31.4	10	2	PT0243	ig heavy chain CRD
34	16	31.4	12	1	UT060	tremorgen A-10 -
35	16	31.4	12	2	S26548	T-cell receptor be
36	16	31.4	12	2	S47391	T-cell antigen rec
37	16	31.4	12	2	S47394	T-cell antigen rec
38	16	31.4	12	2	S47395	T-cell antigen rec
39	16	31.4	13	2	S63492	dissimilatory sul
40	16	31.4	13	2	PT0263	ig heavy chain CRD
41	16	31.4	13	2	PT0304	ig heavy chain CRD
42	16	31.4	14	2	IS1430	hemoglobin beta ch
43	16	31.4	14	2	PH1586	ig H chain V-D-J r
44	15	29.4	8	2	S37141	psa protein - Erv
45	15	29.4	8	2	PH1618	ig H chain V-D-J r

ALIGNMENTS

RESULT 1
PT0331
IG heavy chain CRD3 region (clone J2-121) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_rev1510337; PMID:1899102
C/Accession: PT0331
R/Yamada, M.; Maserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A/Reference number: PT0222; MUID:9108337; PMID:1899102
A/Accession: PT0331
A/Molecule type: DNA
A/Residues: 1-13 <YAM>
A:Experimental source: B lymphocyte
C/Keywords: heterotetramer; immunoglobulin

Query Match 45.1%; Score 23; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GYKNSKF 9
DB 6 GYNNPF 12

RESULT 2
S36678
dodecenoyl-CoA Delta-isomerase (EC 5.3.3.8) / enoyl-CoA hydratase (EC 4.2.1.17) / 3-hydr
C/Species: Mus musculus (house mouse)
C/Date: 19-Mar-1997 #sequence_rev1510337; PMID:1899102
C/Accession: S36678
R/Chen, N.; Crane, D.I.
Biochem. J. 281, 605-610, 1992
A/Title: Induction of the major integral membrane protein of mouse liver peroxisomes by
A/Reference number: S21285; MUID:92246895; PMID:1555703
A/Accession: S36678
A/Molecule type: protein
A/Residues: 1-14 <CHE>
A:Experimental source: liver
C/Function:
A/Pathway: fatty acid beta-oxidation
C/Keywords: carbon-oxygen lyase; fatty acid beta-oxidation; hydro-lyase; intramolecular

Query Match 45.1%; Score 23; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 FGYNKSKF 9
DB 1 FGYNKSKF 8

RESULT 3
 PH1454
 T-cell receptor alpha chain (clone A3/72.2) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
 C/Accession: PH1454
 R/Casanova, J.L.; Martignon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Kd
 U. Exp. Med. 177, 811-820, 1993
 A>Title: T cell receptor selection by and recognition of two class I major histocompatib
 A:Reference number: PH1430; MUID:93171821; PMID:8436911
 A/Accession: PH1454
 A:Molecule type: mRNA
 A:Residues: 1-12 <CAS>
 A:Experimental source: cytolytic T-lymphocyte
 C:Superfamily: immunoglobulin homology
 C:Keywords: receptor; T-cell

Query Match 43.1%; Score 22; DB 2; Length 12;
 Best Local Similarity 57.1%; Pred. No. 5.6e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 GYKNSKF 9
 DB 5 GYQNFYF 11

RESULT 4

PH0787
 T-cell receptor alpha chain (F8) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C/Accession: PH0787
 R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
 J. Exp. Med. 174, 1371-1383, 1991
 A>Title: T cell receptor genes in a series of class I major histocompatibility complex-I
 allelic exclusion and antigen-specific repertoire.
 A:Reference number: PH0746; MUID:92078846; PMID:1836010
 A/Accession: PH0787
 A:Molecule type: mRNA
 A:Residues: 1-13 <CAS>
 A:Cross-references: EMBL:X60891
 A:Experimental source: T lymphocyte
 C:Keywords: T-cell receptor

Query Match 43.1%; Score 22; DB 2; Length 13;
 Best Local Similarity 57.1%; Pred. No. 5.1e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 GYKNSKF 9
 DB 6 GYQNFYF 12

RESULT 5

PC4373
 telomeric and tetraplex DNA binding protein qTBP42 III - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 07-May-1999
 C/Accession: PC4373
 R/Satig, G.; Weisman-Shomer, P.; Fry, M.
 Biochem. Biophys. Res. Commun. 237, 617-623, 1997
 A>Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the CA
 A:Reference number: PC4371; MUID:97445086; PMID:9299414
 A/Accession: PC4373
 A:Molecule type: protein
 A:Residues: 1-8 <SAR>
 C:Comment: This protein binds either strand of the telomeric DNA as well as unimolecular
 F1-4/Domain: RNPI #status predicted <RNP>

Query Match 41.2%; Score 21; DB 2; Length 8;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGY 4
 DB 1 GFGF 4

RESULT 6

JP0073
 ribosomal protein L32 - Leuconostoc mesenteroides (fragment)
 C:Species: Leuconostoc mesenteroides
 C>Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 28-Oct-1994
 A/Accession: JP0073
 R/Ochi, K.
 Submitted to JIPD, February 1994
 A:Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal pro
 A:Reference number: JP0042
 A/Accession: JP0073
 A:Molecule type: protein
 A:Residues: 1-9 <OCH>
 C:Keywords: protein biosynthesis; ribosome

Query Match 39.2%; Score 20; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KNSK 8
 DB 6 KNSK 9

RESULT 7

B33995
 hypothalamic hormone - black horse fly
 C:Species: Tabanus atratus (black horse fly)
 C>Date: 22-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 31-Oct-1997
 C/Accession: B33995
 R/Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhang, Y
 Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989
 A>Title: Primary structure of two neuropeptide hormones with adipokinetic and hypothalamic
 A:Reference number: A33995; MUID:90046758; PMID:2813385
 A/Accession: B33995
 A:Molecule type: protein
 A:Residues: 1-10 <UAF>
 C:Superfamily: adipokinetic hormone
 C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
 F1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
 F10/Modified site: amidated carboxyl end (Tyr) #status predicted

Query Match 39.2%; Score 20; DB 2; Length 10;
 Best Local Similarity 75.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGY 4
 DB 7 GFGY 10

RESULT 8

PT0211
 T-cell receptor alpha chain V-J region (4-1-G.4) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
 C/Accession: PT0211
 R/Nakano, N.; Kikuchi, H.; Nishimoto, H.; Kishimoto, T.
 J. Exp. Med. 173, 1091-1097, 1991
 A>Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restrict
 A:Reference number: PT0209; MUID:91211721; PMID:1902501
 A/Accession: PT0211
 A:Molecule type: mRNA
 A:Residues: 1-11 <NAK>
 C:Keywords: T-cell receptor

Query Match 39.2%; Score 20; DB 2; Length 11;
 Best Local Similarity 75.0%; Pred. No. 1.2e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYKN 6
||:|
DB 8 GYQN 11

RESULT 9

S38307
DB: A protein - fruit fly (*Drosophila melanogaster*) (fragment)
C/Species: *Drosophila melanogaster*
C/Date: 19-May-1994 #sequence_revision 27-Feb-1997 #text_change 17-Mar-1999
C/Accession: S38307
R/Wang, G.L.; Goldstein, B.S.
Biochim. Biophys. Acta 1216, 94-104, 1993
A/Title: An AP-1 binding site in the upstream region of DBB-A is part of a developmental
A/Reference number: S38307; MUID:94032494; PMID:8218421
A/Accession: S38307
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-14 <MAN>

Query Match 39.2%; Score 20; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FGYNK 7
|||
DB 4 FGYS 9

RESULT 10

B61033
zanatachykinin B - bullfrog
C/Species: *Rana catesbeiana* (bullfrog)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000
C/Accession: B61033; J00427
R.Kangawa, K.; Kozawa, H.; Hino, J.; Minamino, N.; Matsuo, H.
Regul. Pept. 42(Suppl.1), S12, 1992
A/Title: Isolation of four novel tachykinins from frog (*Rana catesbeiana*) brain and inte
A/Reference number: A61033
A/Accession: B61033
A/Molecule type: protein
A/Residues: 1-10 <KAN>
R.Kozawa, H.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 177, 588-595, 1991
A/Title: Isolation of four novel tachykinins from frog (*Rana catesbeiana*) brain and inte
A/Reference number: J00426; MUID:91554357; PMID:2043143
A/Accession: J00427
A/Molecule type: protein
A/Residues: 1-10 <KOZ>
C/Superfamily: unassigned animal peptides
C/Keywords: amidated carboxyl end; neuropeptide
F/10/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 37.3%; Score 19; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 YKNSKF 9
||:|
DB 1 YKSDSF 6

RESULT 11

B58502
36K kidney stone protein - unidentified bacterium (fragment)
C/Species: unidentified bacterium
C/Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
C/Accession: B58502
R.Binette, J.P.; Binette, M.B.
Submitted to the Protein Sequence Database, October 1996
A/Description: The proteins of kidney and gallbladder stones.

A/Reference number: A58501
A/Accession: B58502

A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-14 <BIN>
A/Experimental source: human kidney stone containing Ca ox.monoc dihyd, 1* survive, CAP
A/Note: tentative identification of 8-Tyr and 9-Tyr

Query Match 37.3%; Score 19; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FGY 4
|||
DB 6 FGY 8

RESULT 12

PC7074
translation elongation factor eEF-1 beta chain - mouse (fragment)
C/Species: *Mus musculus* (house mouse)
C/Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C/Accession: PC7074
R.Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.;
Electrophoresis 21, 1853-1871, 2000
A/Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of t
A/Reference number: PC7072
A/Accession: PC7074
A/Molecule type: protein
A/Residues: 1-9 <TSU>
A/Experimental source: strain C57BL/6Cr Slc, male; brain, cortex
C/Keywords: brain; cerebral cortex

Query Match 35.3%; Score 18; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFG 3
|||
DB 1 GFG 3

RESULT 13

F60527
sperm-activating peptide (Gly-3,5 SAP-I) - sea urchin (*Tripteneustes gratilla*)
N/Alternate names: speract homolog TG-8
C/Species: *Tripteneustes gratilla*
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C/Accession: F60527; H39572
R.Yoshino, K.I.; Kajitara, H.; Nomura, K.; Takao, T.; Shimomichi, Y.; Kurita, M.; Yamaguc
Comp. Biochem. Physiol. B 94, 739-751, 1989
A/Title: A halogenated amino acid-containing sperm activating peptide and its related pe
ocus nudus, *Echinometra mathaei* and *Heterocentrotus mammillatus*.
A/Reference number: A60527
A/Accession: F60527

A/Molecule type: protein
A/Residues: 1-10 <YOS>
A/Note: this peptide did not contain bromophenylalanine
R.Yoshino, K.; Takao, T.; Suhara, M.; Kitai, T.; Hori, H.; Nomura, K.; Yamaguchi, M.; St
Biochemistry 30, 6203-6209, 1991
A/Title: Identification of a novel amino acid, o-bromo-L-phenylalanine, in egg-associated
A/Reference number: A39572; MUID:91283461; PMID:2059627
A/Accession: H39572
A/Molecule type: protein
A/Residues: 1-10 <YOS>
A/Note: this peptide contained bromophenylalanine
C/Superfamily: unassigned animal peptides
C/Keywords: bromine
F/2/Modified site: 2'-bromophenylalanine (Phe) (partial) #status experimental

Query Match 35.3%; Score 18; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFG 3
|||
Db 1 GFG 3

RESULT 14

B60589
sperm-activating peptide (Gly-3, Ser-5, Ile-9 SAB-I) - slate-pencil urchin (Heterocentrus
C/Species: Heterocentrus mamilatus
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2000
C/Accession: B60589
R/Oshino, K.I.; Kajima, H.; Nomura, K.; Takao, T.; Shimomishi, Y.; Kurita, M.; Yamaguchi
Comp. Biochem. Physiol. B 94, 739-751, 1989
A/Title: A halogenated amino acid-containing sperm activating peptide and its related pe
otus nudus, Echinosmeta mathaei and Heterocentrus mamilatus.
A/Reference number: A60527
A/Accession: B60589
A/Molecule type: protein
A/Residues: 1-10 <YOS>
C/Superfamily: unassigned animal peptides

Query Match 35.3%; Score 18; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFG 3
|||
Db 1 GFG 3

RESULT 15

S06964
hypothetical protein (nifa 5' region) - Rhizobium leguminosarum (fragment)
C/Species: Rhizobium leguminosarum
C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 08-Oct-1999
C/Accession: S06964
R/Roeijink, P.W.; Hontelez, J.G.J.; van Kammen, A.; van den Bos, R.C.
Mol. Microbiol. 3, 1441-1447, 1989
A/Title: Nucleotide sequence of the regulatory nifa gene of Rhizobium leguminosarum PRB
A/Reference number: S06964; MUID:90136072; PMID:2693897
A/Accession: S06964
A/Molecule type: DNA
A/Residues: 1-10 <ROES>
A/Cross-references: EMBL:X17073; NID:G46208; PIDN:CAA34923.1; PID:G809748

Query Match 35.3%; Score 18; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFG 3
|||
Db 3 GFG 5

RESULT 16

P00753
beta-fructofuranosidase (EC 3.2.1.26) IIB - barley (fragment)
C/Species: Hordeum vulgare (barley)
C/Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 23-Mar-1995
C/Accession: P00753
R/Oberland, D.M.; Simmen, U.; Bollner, T.; Wiemken, A.
Plant Physiol. 101, 1331-1339, 1993
A/Title: Purification and characterization of three soluble invertases from barley (Hor
A/Reference number: P00752; MUID:94143483; PMID:8310063
A/Accession: P00753
A/Molecule type: protein
A/Residues: 1-10 <OBE>
A/Experimental source: leaf, cv. Express
C/Keywords: alternative initiators; glycoprotein; glycosidase; hydrolase

Query Match 35.3%; Score 18; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 2.7e+03;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 GFGYNS 7
|||
Db 1 GPFMDNT 7

RESULT 17

A44755
20alpha-hydroxysteroid dehydrogenase (EC 1.1.1.149) - Clostridium scindens (fragment)
C/Species: Clostridium scindens
C/Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 17-Mar-1999
C/Accession: A44755
R/Krafft, A.E.; Hylemon, P.B.
J. Bacteriol. 171, 2925-2932, 1989
A/Title: Purification and characterization of a novel form of 20alpha-hydroxysteroid dehy
A/Reference number: A44755; MUID:89255043; PMID:2722736
A/Accession: A44755
A/Molecule type: protein
A/Residues: 1-11 <KRA>
C/Comment: This enzyme was purified to homogeneity and shown to have 20alpha hydroxyster
sphate dehydrogenase (GAPDH) activity although the fragment shows near identity to known
C/Keywords: homotetramer; NAD; NADP; oxidoreductase

Query Match 35.3%; Score 18; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFG 3
|||
Db 8 GFG 10

RESULT 18

S26547
T-cell receptor beta chain (clone Cw3/10.1) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
C/Accession: S26547
R/Casanova, J.L.; Gerotini, J.C.; Matches, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A/Reference number: S26547; MUID:92364546; PMID:1380061
A/Accession: S26547
A/Molecule type: mRNA
A/Residues: 1-12 <CAS>
A/Cross-references: EMBL:X67997
A/Experimental source: cytolytic T-lymphocyte, clone Cw3/10.1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: T-cell receptor

Query Match 35.3%; Score 18; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGY 4
|||
Db 6 GFDY 9

RESULT 19

PT0274
Ig heavy chain CRD3 region (clone 3-109B) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C/Accession: PT0274
R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shale, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A/Reference number: PT0222; MUID:91108337; PMID:1899102
A/Accession: PT0274
A/Molecule type: DNA
A/Residues: 1-12 <YAM>

A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 35.3%; Score 18; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GYKS 7
|||
Db 2 GYSS 6

RESULT 20

VCAM-1 5'UTR binding protein - Rana pipiens (fragment)

C:Species: Rana pipiens

C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001

C:Accession: A59387

R:BANBRUE, H.

Submitted to the Protein Sequence Database, February 2001

A:Description: Identification and characterization of a novel VCAM-1 5'UTR.

A:Reference number: A59387

A:Accession: A59387

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <BAN>

A:Experimental source: CCL-145

A>Note: VCAM-1 5' untranslated region binding protein with a probable translation inhibi

Query Match 35.3%; Score 18; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYK 5
|||
Db 8 GYK 10

RESULT 21

glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - rice (strain

PS0277

C:Species: Oryza sativa (rice)

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 03-Jun-2002

C:Accession: PS0277

R:Tsuigita, A.

Submitted to JIPID, April 1993

A:Reference number: PS0206

A:Accession: PS0277

A:Molecule type: protein

A:Residues: 1-13 <TSU>

A:Experimental source: leaf, chlorophyll, stem

C:Keywords: oxidoreductase

Query Match 35.3%; Score 18; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFG 3
|||
Db 9 GFG 11

RESULT 22

IS1432

histone H4-1 precursor - African clawed frog (fragment)

C:Species: Xenopus laevis (African clawed frog)

C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999

C:Accession: IS1432

R:Gargiulo, G.; Razvi, F.; Ruberti, I.; Mohr, I.; Worcel, A.

J. Mol. Biol. 181, 333-349, 1985

A>Title: Chromatin-specific hypersensitive sites are assembled on a Xenopus histone gene

A:Reference number: IS1431; PMID:8510855; PMID:4039007

A:Accession: IS1432

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 114 <GB>

A:Cross-references: GB:M23777; NID:G214219; PIDN:AAA49737.1; PID:G214222

C:Superfamily: histone H4

Query Match 35.3%; Score 18; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFG 3
|||
Db 11 GFG 13

RESULT 23

glucose 1-dehydrogenase (NAD) (EC 1.1.1.118) - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 03-Jun-2002

C:Accession: A17150

R:Franzen, B.; Carrubba, C.; Feingold, D.S.; Ashcom, J.; Franzen, J.S.

Biochem. J. 199, 599-602, 1981

A>Title: Amino acid sequence of the tryptic peptide containing the catalytic-site thiol

A:Reference number: A17150; PMID:82182061; PMID:6896145

A:Accession: A17150

A:Molecule type: protein

A:Residues: 1-14 <FRA>

C:Keywords: NAD; oxidoreductase

Query Match 35.3%; Score 18; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFG 3
|||
Db 4 GFG 6

RESULT 24

acetyl ornithine decarboxylase (argE) - Escherichia coli (fragment)

C:Species: Escherichia coli

C>Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 08-Oct-1999

C:Accession: I41138

R:Charlier, D.; Piette, J.; Glansdorff, N.

Nucleic Acids Res. 10, 5935-5948, 1982

A>Title: arg can function as a mobile promoter in e.coli.

A:Reference number: I41137; PMID:83064529; PMID:6292860

A:Accession: I41138

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-11 <RES>

A:Cross-references: GB:J01589; NID:G145346; PIDN:AAA23485.1; PID:G551788

Query Match 33.3%; Score 17; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGY 4
|||
Db 8 GTGY 11

RESULT 25

spermadhesin AQN-3 - pig (fragments)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 17-Mar-1999

C:Accession: S68649

R:Calvete, J.J.; Postlova, Z.; Sanz, L.; Adertmann, K.; Thole, H.H.; Toepfer-Petersen, E

FEBS Lett. 379, 207-211, 1996

A>Title: Mapping the heparin-binding domain of boar spermadhesins.

A:Reference number: S68648; MUID:96184566; PMID:8603690
 A:Accession: S68649
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-67-11 <CAL>

Query Match 33.3%; Score 17; DB 2; Length 11;
 Best Local Similarity 42.9%; Pred. No. 4.5e+03;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKNS 7
 |||||
 Db 5 GWYQSS 11

RESULT 26

PH0939
 T-cell receptor beta chain V-D-J region (clone 10) - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)
 C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
 C:Accession: PH0939
 R:Gold: D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
 J. Exp. Med. 176, 1467-1476, 1991
 A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy
 A:Reference number: PH0891; MUID:92078857; PMID:1836012
 A:Accession: PH0939
 A:Molecule type: mRNA
 A:Residues: 1-11 <SOL>
 A:Experimental source: complete Freund's adjuvant-immunized lymph node
 C:Keywords: T-cell receptor

Query Match 33.3%; Score 17; DB 2; Length 11;
 Best Local Similarity 60.0%; Pred. No. 4.5e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GYKNS 7
 |||||
 Db 7 GLKNT 11

RESULT 27

A61361
 bradykinin-like peptide - Bombina orientalis

C:Species: Bombina orientalis
 C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 18-Aug-2000
 C:Accession: A61361
 R:Yasuhara, T.; Hira, M.; Nakajima, T.; Yanaiharu, N.; Yanaiharu, C.; Hashimoto, T.; Sak
 Chem. Pharm. Bull. 21, 1388-1391, 1973
 A:Title: Active peptides on smooth muscle in the skin of Bombina orientalis Boulenger an
 A:Reference number: A61361; MUID:73256822; PMID:4732297
 A:Accession: A61361
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-13 <YAS>
 C:Superfamily: unassigned animal peptides
 C:Keywords: skin

Query Match 33.3%; Score 17; DB 2; Length 13;
 Best Local Similarity 44.4%; Pred. No. 5.3e+03;
 Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GFGYKNSK 9
 |||||
 Db 4 GFSPRGKF 12

RESULT 28

PH1597
 Ig H chain V-D-J region (wild-type clone 304) - mouse (fragment)

C:Species: Mus musculus (house mouse)
 C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C:Accession: PH1597
 R:Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993
 A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A:Reference number: PH1580; MUID:93301609; PMID:8315387
 A:Accession: PH1597
 A:Molecule type: DNA
 A:Residues: 1-14 <LEV>
 A:Experimental source: bone marrow pre-B lymphocyte
 C:Keywords: immunoglobulin

Query Match 33.3%; Score 17; DB 2; Length 14;
 Best Local Similarity 75.0%; Pred. No. 5.7e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGY 4
 |||||
 Db 5 GSGY 8

RESULT 29

PC7079
 unidentified 27.2K protein - mouse (fragment)

C:Species: Mus musculus (house mouse)
 C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
 C:Accession: PC7079
 R:Teugela, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.; N
 Electrophoresis 21, 1853-1871, 2000
 A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of t
 A:Reference number: PC7072
 A:Accession: PC7079
 A:Molecule type: protein
 A:Residues: 1-14 <TSU>
 A:Experimental source: strain C57BL/6Cr Slc, male; brain, striatum
 C:Keywords: brain

Query Match 33.3%; Score 17; DB 2; Length 14;
 Best Local Similarity 42.9%; Pred. No. 5.7e+03;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 FGYNKSK 8
 |||||
 Db 2 YKYNKSK 8

RESULT 30

C59137
 protein P73 - golden needle mushroom (fragment)

C:Species: Flammulina velutipes (golden needle mushroom)
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: C59137
 R:Sakamoto, Y.; Ando, A.; Tamai, Y.; Miura, K.
 submitted to the Protein Sequence Database, November 1999
 A:Description: Differences of proteins expressed in the fruiting dikaryon and the non-fr
 A:Reference number: A59137
 A:Accession: C59137
 A:Molecule type: protein
 A:Residues: 1-14 <SAK>

Query Match 33.3%; Score 17; DB 2; Length 14;
 Best Local Similarity 75.0%; Pred. No. 5.7e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGY 4
 |||||
 Db 5 GFGY 8

RESULT 31

A42266
 peptidylglycine monooxygenase (EC 1.14.17.3), rPAM-5 - rat (fragment)

N:Alternate names: peptidylglycine alpha-amidating monooxygenase
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 26-May-1995
 C:Accession: A42266

R/Eipper, B.A.; Green, C.B.; Campbell, T.A.; Stoffers, D.A.; Keutmann, H.T.; Mains, R.E.
 J. Biol. Chem. 267, 4008-4015, 1992
 A>Title: Alternative splicing and endoproteolytic processing generate tissue-specific fg
 A/Reference number: A42266; MUID:92156145; PMID:1740449
 A/Accession: A42266
 A/Status: Preliminary
 A/Molecule type: mRNA
 A/Residues: 1-9 <EIP>
 A/Experimental source: pituitary
 A/Note: sequence extracted from NCBI backbone (NCBI:82733, NCBI:82750)
 C/Keywords: oxidoreductase

Query Match 31.4%; Score 16; DB 2; Length 9;
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 3 GYKNS 7
 |||
 Db 4 GFKOT 8

RESULT 32
 C45474
 thrombospondin 2 - bovine (fragment)
 N/Alternate names: corticotropin-induced secreted protein (CISP); thrombospondin homolog
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 14-Aug-1998
 C/Accession: C45474
 R/Pellerin, S.; Lafuillade, B.; Scherrer, N.; Gagnon, J.; Shi, D.L.; Chambaz, E.M.; Fej
 J. Biol. Chem. 268, 4304-4310, 1993
 A>Title: Corticotropin-induced secreted protein, an ACTH-induced protein secreted by ad
 A/Reference number: A45474; MUID:93179438; PMID:8382699
 A/Accession: C45474
 A/Status: Preliminary
 A/Molecule type: protein
 A/Residues: 1-10 <PEL>
 A/Experimental source: adrenocortical cells
 A/Note: sequence extracted from NCBI backbone (NCBI:125844)
 C/Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; VC

Query Match 31.4%; Score 16; DB 2; Length 10;
 Best Local Similarity 66.7%; Pred. No. 6.3e+03;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 FGXY 4
 |||
 Db 2 YGY 4

RESULT 33
 PT0243
 1g heavy chain CRD3 region (clone 2-103A) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C/Accession: PT0243
 R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Royera, G.
 J. Exp. Med. 173, 395-407, 1991
 A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
 A/Reference number: PT0222; MUID:91108337; PMID:1899102
 A/Accession: PT0243
 A/Molecule type: DNA
 A/Residues: 1-10 <YAM>
 A/Experimental source: B lymphocyte
 C/Keywords: heterotetramer; immunoglobulin

Query Match 31.4%; Score 16; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 6.3e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 GYKNS 7
 |||
 Db 2 GYYS 6

RESULT 34
 J7UJ30
 Tremorgen A-10 - jelly fungus (Tremella mesenterica)
 C/Species: Tremella mesenterica
 C/Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 07-Nov-1997
 C/Accession: A01642; A61313
 R/Sakagami, Y.; Yoshida, M.; Isogai, A.; Suzuki, A.
 Science 212, 1525-1527, 1981
 A>Title: Peptide sex hormones inducing conjugation tube formation in compatible mating-ty
 A/Reference number: A94256
 A/Accession: A01642

A/Molecule type: protein
 A/Residues: 1-12 <SAK1>
 A/Note: the farnesyl may instead be (2E,6E,10Z)-12-hydroxyfarnesyl
 R/Sakagami, Y.; Isogai, A.; Suzuki, A.; Tamura, S.; Tsuchiya, E.; Fukui, S.
 Agric. Biol. Chem. 42, 1301-1302, 1978
 A>Title: Amino acid sequence of tremorgen A-10, a peptidal hormone, inducing conjugation
 A/Reference number: A61313
 A/Accession: A61313
 A/Molecule type: Protein
 A/Residues: 1-12 <SAK2>
 C/Comment: Tremorgen A-10 is produced by the A mating-type cells and induces formation
 C/Superfamily: tremorgen A-13
 C/Keywords: extracellular protein; hormone; lipoprotein; methylated carboxyl end; pherom
 F/12/Binding site: farnesyl (Cys) (covalent) #status experimental
 F/12/Modified site: methyl ester carboxyl end (Cys) #status experimental

Query Match 31.4%; Score 16; DB 1; Length 12;
 Best Local Similarity 75.0%; Pred. No. 7.6e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GFXY 4
 |||
 Db 8 GNGY 11

RESULT 35
 S26548
 T-cell receptor beta chain (clone Cw3/Cas3) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
 C/Accession: S26548
 R/Csanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gounnier, H.; Barra, C.; Wid
 J. Exp. Med. 176, 439-447, 1992
 A>Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
 A/Reference number: S26512; MUID:92364546; PMID:1380061
 A/Accession: S26548
 A/Molecule type: mRNA
 A/Residues: 1-12 <CAS>
 A/Cross-references: EMBL:X67998
 A/Experimental source: cytolitic T lymphocytes
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: T-cell receptor

Query Match 31.4%; Score 16; DB 2; Length 12;
 Best Local Similarity 75.0%; Pred. No. 7.6e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GFXY 4
 |||
 Db 6 GGGY 9

RESULT 36
 S47391
 T-cell antigen receptor VJ junction beta chain - human
 C/Species: Homo sapiens (man)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C/Accession: S47391; S47386
 R/Lehner, P.J.
 submitted to the EMBL Data Library, August 1994
 A/Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c

A:Reference number: S47355
 A:Accession: S47391
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-12 <LEH>
 A:Cross-references: EMBL:Z35712; NID:9527519; PIDN:CAA84781.1; PID:9527520; EMBL:Z35701;
 C:Keywords: T-cell receptor

Query Match 31.4%; Score 16; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 7.6e+03;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FGX 4
 :||
 Db 8 YGY 10

RESULT 37

S47394
 T-cell antigen receptor VJ junction beta chain - human
 C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C:Accession: S47394; S47369
 R:Lehner, P.J.
 Submitted to the EMBL Data Library, August 1994
 A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T C
 A:Reference number: S47355
 A:Accession: S47394
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-12 <LEH>
 A:Cross-references: EMBL:Z35714; NID:9527523; PIDN:CAA84783.1; PID:9527524; EMBL:Z35694;
 C:Keywords: T-cell receptor

Query Match 31.4%; Score 16; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 7.6e+03;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FGX 4
 :||
 Db 8 YGY 10

RESULT 38

S47395
 T-cell antigen receptor VJ junction beta chain - human
 C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C:Accession: S47395
 R:Lehner, P.J.
 Submitted to the EMBL Data Library, August 1994
 A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T C
 A:Reference number: S47355
 A:Accession: S47395
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-12 <LEH>
 A:Cross-references: EMBL:Z35715; NID:9527525; PIDN:CAA84784.1; PID:9527526
 C:Keywords: T-cell receptor

Query Match 31.4%; Score 16; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 7.6e+03;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FGX 4
 :||
 Db 8 YGY 10

RESULT 39

S63492
 dissimilatory sulfite reductase beta chain, soluble - Desulfovibrio desulfuricans (fragm
 C:Species: Desulfovibrio desulfuricans

C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
 C:Accession: S63492
 R:Seubler, J.; Arendsen, A.F.; Hagen, W.R.; Kroneck, P.M.H.
 Eur. J. Biochem. 233, 873-879, 1995
 A:Title: Molecular properties of the dissimilatory sulfite reductase from Desulfovibrio C
 A:Reference number: S63489; MUID:96085152; PMID:8521853
 A:Accession: S63492
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-13 <STR>

Query Match 31.4%; Score 16; DB 2; Length 13;
 Best Local Similarity 50.0%; Pred. No. 8.2e+03;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GYKSK 8
 :|||
 Db 6 GYNPK 11

RESULT 40

PT0263
 Ig heavy chain CRD3 region (clone 2-121B) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PT0263
 R:Yamada, M.; Masserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J C
 A:Reference number: PT0222; MUID:91108337; PMID:1899102
 A:Accession: PT0263
 A:Molecule type: DNA
 A:Residues: 1-13 <YAM>
 A:Experimental source: B lymphocyte
 C:Keywords: heterodimer; immunoglobulin

Query Match 31.4%; Score 16; DB 2; Length 13;
 Best Local Similarity 75.0%; Pred. No. 8.2e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGY 4
 :|||
 Db 2 GGGY 5

RESULT 41

PT0304
 Ig heavy chain CRD3 region (clone 5-115B) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PT0304
 R:Yamada, M.; Masserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J C
 A:Reference number: PT0222; MUID:91108337; PMID:1899102
 A:Accession: PT0304
 A:Molecule type: DNA
 A:Residues: 1-13 <YAM>
 A:Experimental source: B lymphocyte
 C:Keywords: heterodimer; immunoglobulin

Query Match 31.4%; Score 16; DB 2; Length 13;
 Best Local Similarity 66.7%; Pred. No. 8.2e+03;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FGX 4
 :|||
 Db 2 YGY 4

RESULT 42

IS1430
 hemoglobin beta chain - African clawed frog (fragment)

C/Species: Xenopus laevis (African clawed frog)
 C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 19-May-2000
 C/Accession: 151430
 R/Kay, R.M.; Harris, R.; Patient, R.K.; Williams, J.G.
 Nucleic Acids Res. 8, 2691-2707, 1980
 A/Title: Molecular cloning of cDNA sequences coding for the major alpha- and beta-globin
 A/Reference number: 151428; MUID:81053706; PMID:7001356
 A/Accession: 151430
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-14 <LEV>
 A/Cross-references: GB:M10601; NID:g214211; PIDN:AAA49735.1; PID:g214212
 C/Superfamily: globin, globin homology
 C/Keywords: blood; oxygen carrier

Query Match 31.4%; Score 16; DB 2; Length 14;
 Best Local Similarity 75.0%; Pred. No. 8.8e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGY 4
 |||
 Db 10 GKGY 13

RESULT 43

PH1586
 Ig H chain V-D-J region (wild-type clone 10) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C/Accession: PH1586
 R/Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A/Reference number: PH1580; MUID:93301609; PMID:8315387
 A/Accession: PH1586
 A/Molecule type: DNA
 A/Residues: 1-14 <LEV>
 A/Experimental source: bone marrow pre-B lymphocyte
 C/Keywords: immunoglobulin

Query Match 31.4%; Score 16; DB 2; Length 14;
 Best Local Similarity 66.7%; Pred. No. 8.8e+03;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FGXY 4
 |||
 Db 8 YCY 10

RESULT 44

S37141
 rpsa protein - Erwinia chrysanthemi
 C/Species: Erwinia chrysanthemi
 C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Oct-1999
 C/Accession: S37141
 R/Douville, A.; Toussaint, A.; Faellen, M.
 submitted to the EMBL Data Library, August 1993
 A/Description: Identification of the integration host factor genes of E. chrysanthemi.
 A/Reference number: S37139
 A/Accession: S37141
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-8 <DOU>
 A/Cross-references: EMBL:X74750; NID:g399669; PIDN:CAA52769.1; PID:g581108

Query Match 29.4%; Score 15; DB 2; Length 8;
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 YKNSK 8
 |||
 Db 2 FKSAK 6

RESULT 45

PH1618
 Ig H chain V-D-J region (clone B-less 33) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C/Accession: PH1618
 R/Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A/Reference number: PH1580; MUID:93301609; PMID:8315387
 A/Accession: PH1618
 A/Molecule type: DNA
 A/Residues: 1-8 <LEV>
 A/Experimental source: bone marrow pre-B lymphocyte
 C/Keywords: immunoglobulin

Query Match 29.4%; Score 15; DB 2; Length 8;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFG 3
 |||
 Db 5 GYG 7

Search completed: August 30, 2004, 10:58:48
 Job time: 3.70608 secs

Thu Sep 2 07:41:33 2004

us-09-720-469a-3.aug30.rapb

Page 1

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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:49:45 ; Search time 11.0068 Seconds
(without alignments)
257.253 Million cell updates/sec

Title: US-09-720-469A-3

Perfect score: 51

Sequence: 1 GFQYKNSKF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612938 residues

Total number of hits satisfying chosen parameters: 149443

Minimum DB seq length: 8

Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

Result No.	Score	Query Match	Length	ID	Description
1	30	58.8	14	US-10-421-503-13	Sequence 13, Appl1
2	27	52.9	12	US-09-226-666-4	Sequence 4, Appl1
3	26	51.0	14	US-10-223-313A-642	Sequence 642, App
4	25	49.0	9	US-10-233-313A-542	Sequence 542, App
5	25	49.0	9	US-10-233-313A-680	Sequence 680, App
6	25	49.0	10	US-08-996-140-15	Sequence 15, Appl1
7	25	49.0	12	US-08-876-904A-78	Sequence 78, Appl1
8	25	49.0	12	US-10-226-795-15	Sequence 15, Appl1
9	25	49.0	13	US-09-205-658-263	Sequence 263, App
10	25	49.0	13	US-09-963-683-363	Sequence 363, App
11	25	49.0	14	US-09-791-378-526	Sequence 526, App
12	25	49.0	14	US-09-826-290-313	Sequence 313, App
13	25	49.0	14	US-10-449-829A-28	Sequence 28, Appl1
14	25	49.0	14	US-09-988-493-274	Sequence 274, App
15	25	49.0	14	US-10-014-340-467	Sequence 467, App

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	25	49.0	14	US-10-014-340-468	Sequence 468, App
17	25	49.0	14	US-09-791-377-526	Sequence 526, App
18	25	49.0	14	US-10-255-679-50	Sequence 60, Appl1
19	25	49.0	14	US-10-264-309-240	Sequence 158, App
20	24	47.1	9	US-09-780-053-158	Sequence 10940, A
21	24	47.1	9	US-10-057-475B-10940	Sequence 10940, A
22	24	47.1	15	US-10-154-884B-10940	Sequence 180, App
23	24	47.1	10	US-09-780-053-180	Sequence 304, App
24	24	47.1	10	US-09-780-053-304	Sequence 394, App
25	24	47.1	10	US-09-780-053-394	Sequence 472, App
26	24	47.1	10	US-09-780-053-472	Sequence 472, App
27	24	47.1	10	US-10-319-340-8	Sequence 8, Appl1
28	24	47.1	11	US-10-013-815-35	Sequence 35, Appl1
29	24	47.1	11	US-10-013-815-38	Sequence 38, Appl1
30	23	45.1	8	US-10-014-485A-116	Sequence 116, App
31	23	45.1	8	US-10-387-486-10	Sequence 10, Appl1
32	23	45.1	9	US-09-879-957-63	Sequence 63, Appl1
33	23	45.1	9	US-10-460-512-6	Sequence 6, Appl1
34	23	45.1	9	US-10-460-512-28	Sequence 28, Appl1
35	23	45.1	9	US-10-003-983B-11	Sequence 11, Appl1
36	23	45.1	9	US-10-807-856-63	Sequence 623, App
37	23	45.1	10	US-09-572-270A-623	Sequence 2, Appl1
38	23	45.1	10	US-10-317-550-2	Sequence 28, Appl1
39	23	45.1	12	US-10-302-100B-28	Sequence 12, Appl1
40	23	45.1	12	US-10-474-601-12	Sequence 153, App
41	23	45.1	13	US-10-174-105A-153	Sequence 153, App
42	22	43.1	8	US-10-351-641-919	Sequence 154, App
43	22	43.1	9	US-09-799-250-154	Sequence 235, App
44	22	43.1	9	US-09-799-250-235	Sequence 330, App
45	22	43.1	10	US-09-799-250-330	

ALIGNMENTS

RESULT 1
US-10-421-503-13
; Sequence 13, Application US/10421503
; Publication No. US2004000922A1
GENERAL INFORMATION:
APPLICANT: Moehly-Rosen, Daria
TITLE OF INVENTION: Peptide inhibitors of protein kinase C
FILE REFERENCE: 58600-8210, US01
CURRENT APPLICATION NUMBER: US/10/421, 503
CURRENT FILING DATE: 2003-04-22
PRIOR APPLICATION NUMBER: US 60/374, 530
PRIOR FILING DATE: 2002-04-22
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: fragment derived from SEQ ID NO:6
US-10-421-503-13

Query Match 58.8%; Score 30; DB 15; Length 14;
Best Local Similarity 55.6%; Pred. No. 78;
Matches 5; Conservative 1; Mismatches 3; Gaps 0;
Indels 0;
QY 1 GFQYKNSKF 9
Db 2 GFSTNPEF 10
RESULT 2
US-09-226-666-4
; Sequence 4, Application US/0922666A
; Patent No. US20020077282A1
GENERAL INFORMATION:
APPLICANT: Spacciopoli, Peter
APPLICANT: Rothstein, David W.

```
APPLICANT: Friden, Philip M.
TITLE OF INVENTION: METHOD FOR TREATING CYSTIC FIBROSIS
FILE REFERENCE: 50032/007001
CURRENT APPLICATION NUMBER: US/09/226,666A
CURRENT FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Derived from Homo sapiens
US-09-226-666-4
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Query Match          52.9%; Score 27; DB 9; Length 12;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 2 FGYNKSKF 9
    ||||
DB 5 FGYNKSKF 12
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```
RESULT 3
US-10-239-313A-642
; Sequence 642, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 642
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Clostridium tectani
US-10-239-313A-642
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Query Match          51.0%; Score 26; DB 14; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 5 KNSKF 9
    ||||
DB 5 KNSKF 9
```

```
RESULT 4
US-10-239-313A-542
; Sequence 542, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; FILE REFERENCE: 343 727 - US
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CURRENT APPLICATION NUMBER: US/10/239,313A
CURRENT FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: FR 00/03711
PRIOR FILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: PCT 01/70772
PRIOR FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 697
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 542
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-239-313A-542
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```
Query Match          49.0%; Score 25; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 GFGY 4
    ||||
DB 4 GFGY 7
```

```
RESULT 5
US-10-239-313A-680
; Sequence 680, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 680
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-680
```

```
Query Match          49.0%; Score 25; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 GFGY 4
    ||||
DB 4 GFGY 9
```

```
RESULT 6
US-08-996-140-15
; Sequence 15, Application US/08996140
; Publication No. US20030190318A1
; GENERAL INFORMATION:
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: USHIO, Shimpel
; APPLICANT: KUNIKATA, Toshio
; APPLICANT: KIRIMOTO, Masashi
; TITLE OF INVENTION: INTERLEUKIN-18 RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
```


CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/396,140
FILING DATE: 22-DEC-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 356,426/1996
FILING DATE: 26-DEC-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 52,526/1997
FILING DATE: 21-FEB-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 163,490/1997
FILING DATE: 6-JUN-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 215,490/1997
FILING DATE: 28-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOE=2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
US-08-996-140-15

Query Match 49.0%; Score 25; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGY 4
|||
DB 7 GFGY 10

RESULT 7
US-09-876-904A-78
Sequence 78, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
FILE REFERENCE: TB-2002.00
CURRENT APPLICATION NUMBER: US/09/876,904A
FILING DATE: 2001-06-08
PRIORITY APPLICATION NUMBER: US 60/210,925
FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 78
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide crosslinked
US-09-876-904A-78

Query Match 49.0%; Score 25; DB 10; Length 12;
Best Local Similarity 50.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKNSK 8
|||
DB 2 GYGDNRNK 9

RESULT 8
US-10-226-795-15
Sequence 15, Application US/10226795
Publication No. US20040053865A1
GENERAL INFORMATION:
APPLICANT: WILSON, JULIE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND COMPLEMENTARITY-DETERMINING
TITLE OF INVENTION: REGIONS BINDING TO EBOLA GLYCOPROTEIN
FILE REFERENCE: ARMY 166
CURRENT APPLICATION NUMBER: US/10/226,795
FILING DATE: 2002-11-18
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 40
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 15
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic heavy
US-10-226-795-15

Query Match 49.0%; Score 25; DB 12; Length 12;
Best Local Similarity 66.7%; Pred. No. 5.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGYNKS 7
|||
DB 4 FGYNDA 9

RESULT 9
US-09-205-658-263
Sequence 263, Application US/09205658
Patent No. US20010029617A1
GENERAL INFORMATION:
APPLICANT: Ruykun, Gary
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
FILE REFERENCE: 00786/351004
CURRENT APPLICATION NUMBER: US/09/205,658
FILING DATE: 1998-12-03
PRIORITY APPLICATION NUMBER: 08/857,076
FILING DATE: 1997-05-15
EARLIER APPLICATION NUMBER: 08/888,534
FILING DATE: 1997-07-07
EARLIER APPLICATION NUMBER: US98/10080
FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 328
SOFTWARE: PASCSEQ for Windows Version 4.0
SEQ ID NO 263
LENGTH: 13
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-09-205-658-263

Query Match 49.0%; Score 25; DB 9; Length 13;
Best Local Similarity 66.7%; Pred. No. 6e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKN 6

Db 2 GFGWMTN 7

RESULT 10

US-09-963-693-263
; Sequence 263, Application US/09963693
; Publication No. US2003018164A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: OGG, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/963, 693
; CURRENT FILING DATE: 2001-03-25
; PRIOR APPLICATION NUMBER: US/09/205, 658
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 08/857, 076
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: 08/888, 534
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US98/10080
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 263
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-963-693-263

Query Match 49.0%; Score 25; DB 10; Length 13;
Best Local Similarity 66.7%; Pred. No. 6e+02; 1; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 1;

QY 1 GFGYKN 6
Db 2 GFGWMTN 7

RESULT 11

US-09-791-378-526
; Sequence 526, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: 9195-061-999
; CURRENT APPLICATION NUMBER: US/09/791, 378
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750, 395
; PRIOR FILING DATE: 2000-12-26
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 526
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-378-526

Query Match 49.0%; Score 25; DB 9; Length 14;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGYN 6
Db 9 FGYSN 13

RESULT 12
US-09-826-290-313

; Sequence 313, Application US/09826290
; Patent No. US2002016468A1
; GENERAL INFORMATION:
; APPLICANT: Durham, L. Kathryn
; APPLICANT: Friedmann, David L.
; APPLICANT: Herath, Herath Mudiyanselage Achula Chandrasiri
; APPLICANT: Kimmel, Lida H.
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Potter, David M.
; APPLICANT: Rohlf, Christian
; APPLICANT: Silber, B. Michael
; APPLICANT: Stieger, Thomas R.
; APPLICANT: Sunderland, P. Trey
; APPLICANT: Townsend, Robert Reid
; APPLICANT: White, Frost
; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
; TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826, 290
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/194, 504
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/253, 647
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 14
; TYPE: PRT
; ORGANISM: homo sapien
US-09-826-290-313

Query Match 49.0%; Score 25; DB 9; Length 14;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGYN 6
Db 9 FGYSN 13

RESULT 13
US-10-449-829A-28
; Sequence 28, Application US/10449829A
; Publication No. US20040043425A1
; GENERAL INFORMATION:
; APPLICANT: Terrett, Jonathan Alexander
; APPLICANT: Hall, Ian Philip
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF CHRO
; FILE REFERENCE: 2543-1-029
; CURRENT APPLICATION NUMBER: US/10/449, 829A
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: PCT/GB01/05476
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: P32060GB
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-449-829A-28

Query Match 49.0%; Score 25; DB 12; Length 14;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGYN 6
Db 9 FGYSN 13

Db 9 FGYSN 13

RESULT 14

US-09-988-493-274

; Sequence 274, Application US/09988493

; Publication No. US20030064419A1

; GENERAL INFORMATION:

; APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri

; APPLICANT: O'Hare, Michael John

; APPLICANT: Page, Martin John

; APPLICANT: Parekh, Rajesh Bhikhu

; APPLICANT: Waterfield, Michael Derek

; TITLE OF INVENTION: Proteins, Genes, and Their Use for

; TITLE OF INVENTION: Diagnosis and Treatment of Breast Cancer

; FILE REFERENCE: 2543-1-024

; CURRENT APPLICATION NUMBER: US/09/988,493

; CURRENT FILING DATE: 2002-05-21

; PRIOR APPLICATION NUMBER: PCT/GB01/01219

; PRIOR FILING DATE: 2001-03-20

; PRIOR APPLICATION NUMBER: GB 0006695.1

; PRIOR FILING DATE: 2000-03-20

; PRIOR APPLICATION NUMBER: GB 0007265.2

; PRIOR FILING DATE: 2000-02-24

; NUMBER OF SEQ ID NOS: 308

; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO 274

; LENGTH: 14

; TYPE: PRT

; ORGANISM: homo sapien

US-09-988-493-274

QY 2 FGYSN 6

Db 9 FGYSN 13

Query Match 49.0%; Score 25; DB 12; Length 14;

Best Local Similarity 80.0%; Pred. No. 6.4e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 15

US-10-014-340-467

; Sequence 467, Application US/10014340

; Publication No. US20030064411A1

; GENERAL INFORMATION:

; APPLICANT: Herath, et al

; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including

; TITLE OF INVENTION: Diagnosis and Treatment of Alzheimer's Disease

; FILE REFERENCE: 9195-078

; CURRENT APPLICATION NUMBER: US/10/014,340

; CURRENT FILING DATE: 2001-12-10

; NUMBER OF SEQ ID NOS: 823

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 467

; LENGTH: 14

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-014-340-467

QY 2 FGYSN 6

Db 9 FGYSN 13

Query Match 49.0%; Score 25; DB 12; Length 14;

Best Local Similarity 80.0%; Pred. No. 6.4e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 16

US-10-014-340-468

; Sequence 468, Application US/10014340

; Publication No. US20030064411A1

; GENERAL INFORMATION:

; APPLICANT: Herath, et al

; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including

; TITLE OF INVENTION: Diagnosis and Treatment of Alzheimer's Disease

; FILE REFERENCE: 9195-078

; CURRENT APPLICATION NUMBER: US/10/014,340

; CURRENT FILING DATE: 2001-12-10

; NUMBER OF SEQ ID NOS: 823

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 468

; LENGTH: 14

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-014-340-468

QY 2 FGYSN 6

Db 9 FGYSN 13

Query Match 49.0%; Score 25; DB 12; Length 14;

Best Local Similarity 80.0%; Pred. No. 6.4e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 17

US-09-791-377-526

; Sequence 526, Application US/09791377

; Publication No. US20040110938A1

; GENERAL INFORMATION:

; APPLICANT: Parekh, Rajesh

; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF

; TITLE OF INVENTION: SCHIZOPHRENIA

; FILE REFERENCE: 9195-060-999

; CURRENT APPLICATION NUMBER: US/09/791,377

; CURRENT FILING DATE: 2001-02-23

; PRIOR APPLICATION NUMBER: 09/750,395

; PRIOR FILING DATE: 2000-12-28

; NUMBER OF SEQ ID NOS: 677

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 526

; LENGTH: 14

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-791-377-526

QY 2 FGYSN 6

Db 9 FGYSN 13

Query Match 49.0%; Score 25; DB 12; Length 14;

Best Local Similarity 80.0%; Pred. No. 6.4e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 18

US-10-255-679-60

; Sequence 60, Application US/10255679

; Publication No. US20030069175A1

; GENERAL INFORMATION:

; APPLICANT: BAB, ITAI

; APPLICANT: GAZIT, DAN

; APPLICANT: YU-CHEN, CHEN

; APPLICANT: MOHRAD, ANDRAS

; APPLICANT: SHTEYER, ARIE

; APPLICANT: CHOREV, MICHAEL

; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND PSEUDOPEPTIDES HAVING OSTEOGENIC

; TITLE OF INVENTION: ACTIVITY AND PHARMACEUTICAL COMPOSITIONS CONTAINING THE

; FILE REFERENCE: 331949-140798

; CURRENT APPLICATION NUMBER: US/10/255,679

; CURRENT FILING DATE: 2002-09-27

; PRIOR APPLICATION NUMBER: US/09/150,621

; PRIOR FILING DATE: 1998-09-10

```

; PRIOR APPLICATION NUMBER: PCT/IL97/00087
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 117426
; PRIOR FILING DATE: 1996-03-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 60
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-255-679-60
```

```

Query Match          49.0%; Score 25; DB 14; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GFGY 4
      ||||
DB      2 GFGY 5
```

```

RESULT 19
US-10-264-309-240
; Sequence 240, Application US/10264309
; Publication No. US20040022794A1
; GENERAL INFORMATION:
; APPLICANT: DURHAM, L. KATHRYN
; APPLICANT: FRIEDMAN, DAVID L.
; APPLICANT: HERATH, HERATH
; APPLICANT: KIMMEL, LIDA H.
; APPLICANT: PAREKH, RAJESH B.
; APPLICANT: POTTER, DAVID M.
; APPLICANT: ROHLF, CHRISTIAN
; APPLICANT: SILBER, B. MICHAEL
; APPLICANT: SNYDER, PETER J.
; APPLICANT: SOARES, HOLLY D.
; APPLICANT: STIGER, THOMAS R.
; APPLICANT: SUNDERLAND, P. TREY
; APPLICANT: TOWNSEND, ROBERT R.
; APPLICANT: WHITE, W. FROST
; APPLICANT: WILLIAMS, STEPHEN A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR.
; TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
; FILE REFERENCE: POA-002.01
; CURRENT APPLICATION NUMBER: US/10/264,309
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: 60/326,708
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 491
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 240
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-309-240
```

```

Query Match          49.0%; Score 25; DB 16; Length 14;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 FGYN 6
      ||||
DB      9 FGYN 13
```

```

RESULT 20
US-09-780-053-158
; Sequence 158, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-158
```

```

Query Match          47.1%; Score 24; DB 9; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 GYNSKF 9
      |||||
DB      1 GHNSKF 7
```

```

RESULT 21
US-10-057-475B-10940
; Sequence 10940, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aljun
; APPLICANT: Ordenez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-01440205
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
```

SEQ ID NO 10940
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: LYL484 short MHC HLA A3 class I binding peptide
US-10-057-475B-10940

Query Match 47.1% Score 24; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FGK 5
|||
Db 6 FGK 9

RESULT 22
US-10-154-884B-10940
Sequence 10940, Application US/10154884B
Publication No. US2004000561A1

GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
FILE REFERENCE: 014058-013521US
CURRENT FILING DATE: 2002-05-23
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
Remainder Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 11290
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10940
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: LYL484 short MHC HLA A3 class I binding peptide
US-10-154-884B-10940

Query Match 47.1% Score 24; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FGK 5
|||
Db 6 FGK 9

RESULT 23

US-09-780-053-180
Sequence 180, Application US/09780053
Patent No. US20020102640A1
GENERAL INFORMATION:
APPLICANT: Rene S. Hubert
APPLICANT: Daniel E.H. Afar
APPLICANT: Pia M. Chailita-Eid
APPLICANT: Mary Faris
APPLICANT: Elana Levin
APPLICANT: Steve Chappell Mitchell
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
FILE REFERENCE: 129.5US01
CURRENT FILING DATE: 2001-02-09
PRIOR FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 716
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 180
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-780-053-180

Query Match 47.1% Score 24; DB 9; Length 10;
Best Local Similarity 57.1%; Pred. No. 6.9e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GYNSKF 9
||:|
Db 2 GHONSTP 8

RESULT 24
US-09-780-053-304
Sequence 304, Application US/09780053
Patent No. US20020102640A1
GENERAL INFORMATION:
APPLICANT: Rene S. Hubert
APPLICANT: Daniel E.H. Afar
APPLICANT: Pia M. Chailita-Eid
APPLICANT: Mary Faris
APPLICANT: Elana Levin
APPLICANT: Steve Chappell Mitchell
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
FILE REFERENCE: 129.5US01
CURRENT FILING DATE: 2001-02-09
PRIOR FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 716
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 304
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-780-053-304

Query Match 47.1% Score 24; DB 9; Length 10;
Best Local Similarity 57.1%; Pred. No. 6.9e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GYNSKF 9
||:|
Db 1 GHONSTP 7

RESULT 25
US-09-780-053-399

```
; Sequence 399, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Chailita-Bid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.SUSU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 399
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-399
```

```
Query Match 47.1% Score 24; DB 9; Length 10;
Best Local Similarity 57.1%; Pred. No. 6.9e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 3 GYKNSKF 9
|:|:|
Db 1 GHQNSTF 7
```

```
RESULT 26
US-09-780-053-472
; Sequence 472, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Chailita-Bid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.SUSU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 472
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-472
```

```
Query Match 47.1% Score 24; DB 9; Length 10;
Best Local Similarity 57.1%; Pred. No. 6.9e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 3 GYKNSKF 9
|:|:|
Db 4 GHQNSTF 10
```

```
RESULT 27
US-10-319-340-8
; Sequence 8, Application US/10319340
```

```
; Publication No. US20030144211A1
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; APPLICANT: McEwer, Rodger P.
; APPLICANT: Geng, Jian-Guo
; TITLE OF INVENTION: Peptide Inhibitors of Inflammation Mediated by Selectins
; FILE REFERENCE: CTC 102 CON DIV
; CURRENT APPLICATION NUMBER: US/10/319,340
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: 08/135,319
; PRIOR FILING DATE: 1993-10-12
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 10
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic inhibitory peptide
US-10-319-340-8
```

```
Query Match 47.1% Score 24; DB 14; Length 10;
Best Local Similarity 80.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 4 YKNSX 8
|:|:|
Db 1 YKNSX 5
```

```
RESULT 28
US-10-013-815-35
; Sequence 35, Application US/10013815
; Publication No. US20030105000A1
; GENERAL INFORMATION:
; APPLICANT: Pero, Stephanie
; APPLICANT: Krag, David
; APPLICANT: Oligino, Lynn
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING GHB7
; FILE REFERENCE: VO139/7048 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/013,815
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 60/245,755
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of G7BP-4
US-10-013-815-35
```

```
Query Match 47.1% Score 24; DB 14; Length 11;
Best Local Similarity 80.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 2 FGYN 6
|:|:|
Db 3 FGYN 7
```

```
RESULT 29
US-10-013-815-38
; Sequence 38, Application US/10013815
; Publication No. US20030105000A1
; GENERAL INFORMATION:
; APPLICANT: Pero, Stephanie
; APPLICANT: Krag, David
; APPLICANT: Oligino, Lynn
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING GHB7
; FILE REFERENCE: VO139/7048 (HCL/MAT)
```

CURRENT APPLICATION NUMBER: US/10/013,815
CURRENT FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: US 60/245,755
PRIOR FILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 194
SOFTWARE: Patentin version 3.1
SEQ ID NO: 38
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Variant of G7BP-4
US-10-013-815-38

Query Match 47.1%; Score 24; DB 14; Length 11;
Best Local Similarity 80.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYKN 6
DB 3 GYAN 7

RESULT 30
US-10-014-485A-116
Sequence 116, Application US/10014485A
Publication No. US20020168684A1
GENERAL INFORMATION:
APPLICANT: Cell Signaling Technology, Inc.
APPLICANT: ZHANG, Michael J.
APPLICANT: HUI
APPLICANT: TAN, YI
TITLE OF INVENTION: PRODUCTION OF MOTIF-SPECIFIC AND CONTEXT-INDEPENDENT ANTIBODIES
FILE REFERENCE: CST-138 CIP2
CURRENT APPLICATION NUMBER: US/10/014,485A
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: US 09/148,712
PRIOR FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: US 09/535,364
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 145
SOFTWARE: Patentin version 3.1
SEQ ID NO: 116
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD RES
LOCATION: (5)-(5)
OTHER INFORMATION: PHOSPHORYLATION; serine at position 5 is phosphorylated
US-10-014-485A-116

Query Match 45.1%; Score 23; DB 13; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYKN 7
DB 1 GYKN 5

RESULT 31
US-10-387-486-10
Sequence 10, Application US/10387486
Publication No. US20040001867A1
GENERAL INFORMATION:
APPLICANT: INSTITUT PASTEUR
APPLICANT: CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
TITLE OF INVENTION: VECTORS FOR MOLECULE DELIVERY TO CD11b EXPRESSING CELLS
FILE REFERENCE: B4669A -AD/DBO
CURRENT APPLICATION NUMBER: US/10/387,486
CURRENT FILING DATE: 2003-03-14

PRIOR APPLICATION NUMBER: PCT/EP 01/11315
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: EP 00402562.3
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 10
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: intergenic
US-10-387-486-10

Query Match 45.1%; Score 23; DB 15; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GYNSKF 9
DB 2 GCGNSKF 8

RESULT 32
US-09-879-957-63
Sequence 63, Application US/09879957
Patent No. US20020034755A1
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFMAN, No. US20020034755A1h
APPLICANT: KAY, Brian K.
APPLICANT: FOWLER, Dana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND USING SAME
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 63:

US-09-879-957-63

Query Match 45.1%; Score 23; DB 9; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKN 6
DB 1 GDGYON 6

RESULT 33

US-10-460-512-6
; Sequence 6, Application US/10460512
; Publication No. US20040038271A1
; GENERAL INFORMATION:
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Aya Jakobovits
; APPLICANT: Arthur B. Raitano
; TITLE OF INVENTION: NOVEL C-TYPE LECTIN TRANSMEMBRANE
; FILE REFERENCE: 129.20US11
; CURRENT APPLICATION NUMBER: US/10/460,512
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: US/09/638,203
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/148,935
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-460-512-6

Query Match 45.1%; Score 23; DB 12; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKN 7
DB 3 GFTYKTA 9

RESULT 34

US-10-460-512-28
; Sequence 28, Application US/10460512
; Publication No. US20040038271A1
; GENERAL INFORMATION:
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Aya Jakobovits
; APPLICANT: Arthur B. Raitano
; TITLE OF INVENTION: NOVEL C-TYPE LECTIN TRANSMEMBRANE
; FILE REFERENCE: 129.20US11
; CURRENT APPLICATION NUMBER: US/10/460,512
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: US/09/638,203
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/148,935
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-460-512-28

Query Match 45.1%; Score 23; DB 12; Length 9;

Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKN 7
DB 3 GFTYKTA 9

RESULT 35

US-10-003-983B-11
; Sequence 11, Application US/10003983B
; Publication No. US20030103946A1
; GENERAL INFORMATION:
; APPLICANT: Imperial College Innovations
; APPLICANT: Staus, Hans Josef
; APPLICANT: Amrolia, Persis Jal
; TITLE OF INVENTION: Immunotherapeutic Methods and Molecules
; FILE REFERENCE: ICI 103
; CURRENT APPLICATION NUMBER: US/10/003,983B
; CURRENT FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapien
US-10-003-983B-11

Query Match 45.1%; Score 23; DB 14; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 YNKRKF 9
DB 3 YNNHKE 8

RESULT 36

US-10-807-856-63
; Sequence 63, Application US/10807856
; Publication No. US20040157216A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, Noah
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLER, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/807,856
; FILING DATE: 23-Mar-2004
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,915
; FILING DATE: 03-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistock, S. Leslie
; REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-10-807-856-63

Query Match 45.1% Score 23; DB 16; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKN 6
DB 1 GDGYKN 6

RESULT 37
US-09-572-270A-623
Sequence 623, Application US/09572270A
Publication No. US20030148368A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Inter- complementary peptide listing
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/572,270A
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 1144
SOFTWARE: Protpatent version 1.0
SEQ ID NO 623
LENGTH: 10
TYPE: PRT
ORGANISM: Arabidopsis Thaliana
OTHER INFORMATION: Sequence located in Unknown at 192-201 and may interact with
US-09-572-270A-623

Query Match 45.1% Score 23; DB 10; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKN 6
DB 4 GGGFKN 9

RESULT 38
US-10-317-550-2
Sequence 2, Application US/10317550
Publication No. US20030166034A1
GENERAL INFORMATION:
APPLICANT: Thomas, George
TITLE OF INVENTION: P70-S6K or Related Kinase With
FILE REFERENCE: 4-20793/A/PCT
CURRENT APPLICATION NUMBER: US/10/317,550
CURRENT FILING DATE: 2002-12-12
PRIOR APPLICATION NUMBER: US/09/297,404B
PRIOR FILING DATE: 2002-06-04
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 2
LENGTH: 10
TYPE: PRT
ORGANISM: Oryctolagus cuniculus
US-10-317-550-2

Query Match 45.1% Score 23; DB 14; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKN 6
DB 4 GFGSYN 9

RESULT 39
US-10-302-100B-28
Sequence 28, Application US/10302100B
Publication No. US20040054131A1
GENERAL INFORMATION:
APPLICANT: Ballinger, Marcus
TITLE OF INVENTION: Synthetic Peptides Having FGF Receptor
FILE REFERENCE: 035784/263218
CURRENT APPLICATION NUMBER: US/10/302,100B
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: 09/407,687
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: 60/102,667
PRIOR FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 28
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
OTHER INFORMATION: synthetic peptide
US-10-302-100B-28

Query Match 45.1% Score 23; DB 12; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 YKNSKP 9
DB 2 YENSPF 7

RESULT 40
US-10-474-601-12
Sequence 12, Application US/10474601
Publication No. US20040158061A1
GENERAL INFORMATION:
APPLICANT: Friedrich, Thomas
APPLICANT: Stummer, Norbert
TITLE OF INVENTION: Reaction of (di)amines in the presence
FILE REFERENCE: BGI-15605
CURRENT APPLICATION NUMBER: US/10/474,601
CURRENT FILING DATE: 2003-10-09
PRIOR APPLICATION NUMBER: PCT/EP02/03873
PRIOR FILING DATE: 2003-10-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 12
TYPE: PRT
ORGANISM: Pichia pastoris
NAME/KEY: VARIANT
LOCATION: 8
OTHER INFORMATION: Xaa = Any Amino Acid, probably Ser
FEATURE:
NAME/KEY: VARIANT
LOCATION: 11
OTHER INFORMATION: Xaa = Phe or Glu

US-10-474-601-12

Query Match 45.1%; Score 23; DB 16; Length 12;
 Best Local Similarity 42.9%; Pred. No. 1.3e+03;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 GYKSKF 9
 |||:
 Db 1 GYFNAEY 7

RESULT 41

US-10-174-105A-153

Sequence 153, Application US/10174105A

Publication No. US20030068652a1

GENERAL INFORMATION:

APPLICANT: Cell Signaling Technology, Inc.

APPLICANT: ZHANG, Hui

APPLICANT: COMB, Michael J.

APPLICANT: TAN, Yi

TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIFIC,

TITLE OF INVENTION: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCHING,

FILE REFERENCE: CST-138 CIP3

CURRENT APPLICATION NUMBER: US/10/174,105A

CURRENT FILING DATE: 2002-06-18

PRIOR APPLICATION NUMBER: US 09/148,712

PRIOR FILING DATE: 1998-09-04

PRIOR APPLICATION NUMBER: US 09/535,364

PRIOR FILING DATE: 2000-03-24

NUMBER OF SEQ ID NOS: 193

SOFTWARE: PatentIn version 3.1

SEQ ID NO 153

LENGTH: 13

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Synthetic Peptide

FEATURE:

NAME/KEY: MOD_RES

LOCATION: (8)..(8)

OTHER INFORMATION: PHOSPHORYLATION; serine at position 8 is phosphorylated

US-10-174-105A-153

Query Match 45.1%; Score 23; DB 14; Length 13;
 Best Local Similarity 80.0%; Pred. No. 1.4e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYKNS 7
 |||:
 Db 4 GYKNS 8

RESULT 42

US-10-351-641-919

Sequence 919, Application US/10351641

Publication No. US20030186874a1

GENERAL INFORMATION:

APPLICANT: Barney, S.

APPLICANT: Guichie, K.

APPLICANT: Merutka, G.

APPLICANT: Arner, M.

APPLICANT: Lambert, D.

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

TITLE OF INVENTION: PROPERTIES

FILE REFERENCE: 7872-100

CURRENT APPLICATION NUMBER: US/10/351,641

CURRENT FILING DATE: 2003-01-24

PRIOR APPLICATION NUMBER: 09/350,641

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: 09/315,304

PRIOR FILING DATE: 1999-05-20

PRIOR APPLICATION NUMBER: 09/082,279

PRIOR FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1757
 SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 919

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-10-351-641-919

Query Match 43.1%; Score 22; DB 14; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.2e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGY 4
 |||:
 Db 4 GYGY 7

RESULT 43

US-09-799-250-154

Sequence 154, Application US/09799250

Publication No. US20030032087a1

GENERAL INFORMATION:

APPLICANT: Pia M. Challita-Eid

APPLICANT: Rene S. Hubert

APPLICANT: Steve Chappell Mitchell

APPLICANT: Arthur B. Raitano

APPLICANT: Mary Faris

APPLICANT: Daniel E.H. Afar

APPLICANT: Aya Jakobovits

TITLE OF INVENTION: 121P1: A TISSUE SPECIFIC PROTEIN

TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS

FILE REFERENCE: 129.34US01

CURRENT APPLICATION NUMBER: US/09/799,250

CURRENT FILING DATE: 2001-02-08

NUMBER OF SEQ ID NOS: 719

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 154

LENGTH: 9

TYPE: PRT

ORGANISM: Homo sapiens

US-09-799-250-154

Query Match 43.1%; Score 22; DB 10; Length 9;
 Best Local Similarity 42.9%; Pred. No. 1.2e+06;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGKNSK 8
 |||:
 Db 2 FGFEENK 8

RESULT 44

US-09-799-250-235

Sequence 235, Application US/09799250

Publication No. US20030032087a1

GENERAL INFORMATION:

APPLICANT: Pia M. Challita-Eid

APPLICANT: Rene S. Hubert

APPLICANT: Steve Chappell Mitchell

APPLICANT: Arthur B. Raitano

APPLICANT: Mary Faris

APPLICANT: Daniel E.H. Afar

APPLICANT: Aya Jakobovits

TITLE OF INVENTION: 121P1: A TISSUE SPECIFIC PROTEIN

TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS

FILE REFERENCE: 129.34US01

CURRENT APPLICATION NUMBER: US/09/799,250

CURRENT FILING DATE: 2001-02-08

NUMBER OF SEQ ID NOS: 719

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 235

```

; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-250-235

```

```

Query Match 43.1% Score 22; DB 10; Length 9;
Best Local Similarity 42.9% Pred. No. 1.2e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 2 FGYNKSK 8
||: :|
Db 3 FGFEENK 9

```

```

RESULT 45
US-09-799-250-330
; Sequence 330; Application US/09799250
; Publication No. US20030032087A1
; GENERAL INFORMATION:
; APPLICANT: Pia M. Chailica-Eid
; APPLICANT: Rene S. Hubert
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Arthur B. Raitano
; APPLICANT: Mary Paris
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 121P1: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.340801
; CURRENT APPLICATION NUMBER: US/09/799, 250
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 719
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 330
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-250-330

```

```

Query Match 43.1% Score 22; DB 10; Length 9;
Best Local Similarity 42.9% Pred. No. 1.2e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 2 FGYNKSK 8
||: :|
Db 3 FGFEENK 9

```

Search completed: August 30, 2004, 11:04:55
Job time : 13.0068 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:59 ; Search time 3.55743 Seconds
(without alignments)
130.609 Million cell updates/sec

Title: US-09-720-469A-3
Perfect score: 51
Sequence: 1 GFGYKNSKF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 369414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 78885

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgm2_6/ptodata/2/1aa/5A_COMB.pep: *
2: /cgm2_6/ptodata/2/1aa/5B_COMB.pep: *
3: /cgm2_6/ptodata/2/1aa/6A_COMB.pep: *
4: /cgm2_6/ptodata/2/1aa/6B_COMB.pep: *
5: /cgm2_6/ptodata/2/1aa/PTUS_COMB.pep: *
6: /cgm2_6/ptodata/2/1aa/backfiles.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	58.8	12	4	US-09-347-926-13
2	27	52.9	8	1	US-08-320-373-76
3	27	52.9	12	2	US-08-973-563A-28
4	27	52.9	12	2	US-08-973-559-28
5	27	52.9	12	3	US-08-993-235-8
6	27	52.9	12	4	US-09-226-666-4
7	27	52.9	12	4	US-08-993-235-8
8	27	52.9	14	3	US-09-613-182-2
9	25	49.0	10	4	US-09-649-063-15
10	25	49.0	14	4	US-09-150-621-60
11	24.5	48.0	12	2	US-08-973-563A-25
12	24.5	48.0	12	2	US-08-973-559-25
13	24.5	48.0	12	2	US-08-973-559-27
14	24.5	48.0	12	2	US-08-973-559-27
15	24.5	48.0	12	3	US-08-993-235-5
16	24.5	48.0	12	3	US-08-993-235-7
17	24.5	48.0	12	4	US-08-993-235-5
18	24.5	48.0	12	4	US-08-993-235-7
19	24	47.1	9	4	US-09-417-608A-66
20	24	47.1	9	6	5217869-104
21	24	47.1	10	4	US-08-135-319A-8
22	24	47.1	11	4	US-09-383-667-29
23	24	47.1	12	4	US-09-347-926-9
24	23.5	46.1	9	6	5217869-103
25	23	45.1	9	1	US-08-215-805A-3
26	23	45.1	9	1	US-08-215-805A-41
27	23	45.1	9	4	US-08-630-915A-63

28	23	45.1	9	4	US-09-638-203-6	Sequence 6, Appl
29	23	45.1	9	4	US-09-638-203-28	Sequence 28, Appl
30	23	45.1	9	6	5217869-115	Patent No. 5217869
31	23	45.1	11	3	US-08-855-958-4	Sequence 4, Appl
32	23	45.1	11	3	US-08-855-958-9	Sequence 9, Appl
33	23	45.1	12	4	US-09-407-687-28	Sequence 28, Appl
34	23	45.1	14	3	US-09-254-733-50	Sequence 50, Appl
35	22	43.1	8	1	US-08-310-422A-14	Sequence 14, Appl
36	22	43.1	8	2	US-08-690-734A-13	Sequence 13, Appl
37	22	43.1	8	2	US-08-031-538-30	Sequence 30, Appl
38	22	43.1	8	3	US-08-742-185-13	Sequence 13, Appl
39	22	43.1	8	3	US-09-082-279B-919	Sequence 919, Appl
40	22	43.1	8	4	US-09-315-304B-919	Sequence 919, Appl
41	22	43.1	8	4	US-09-834-784-919	Sequence 919, Appl
42	22	43.1	8	4	US-09-515-965A-919	Sequence 919, App
43	22	43.1	8	4	US-09-350-641C-919	Sequence 919, App
44	22	43.1	10	3	US-08-467-580-31	Sequence 31, Appl
45	22	43.1	10	3	US-08-990-015-7	Sequence 7, Appl

ALIGNMENTS

```
RESULT 1
US-09-347-926-13
; Sequence 13, Application US/09347926
; Patent No. 6440386
; GENERAL INFORMATION:
; APPLICANT: LEUNG, SHUI-ON
; TITLE OF INVENTION: STABILIZED RADIOPHOSPHATE-LABELLED PROTEINS
; FILE REFERENCE: 018733/0936
; CURRENT APPLICATION NUMBER: US/09/347, 926
; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ. ID NOS.: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-347-926-13

Query Match      58.8%; Score 30; DB 4; Length 12;
Best Local Similarity 55.6%; Pred. No. 22;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Cy      1 GFGYKNSKF 9
Db      4 GFGYTNPEF 12

RESULT 2
US-08-320-373-76
; Sequence 76, Application US/08320373
; Patent No. 5559025
; GENERAL INFORMATION:
; APPLICANT: Ahorn, Horst
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Sommergruber, Wolfgang
; APPLICANT: Zophel, Andreas
; APPLICANT: Blas, Dieter
; APPLICANT: Kuchler, Ernst
; APPLICANT: Liebig, Hans-Dieter
; APPLICANT: Skern, Timothy
; TITLE OF INVENTION: Expression of Mature Proteinase 2A, the
; TITLE OF INVENTION: Partial Purification Therect and Preparation of Substrates
; TITLE OF INVENTION: Having an Inhibitory Effect
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
```

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; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,373
; FILING DATE: 11-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/971,619
; FILING DATE: 06-NOV-1992
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 466-0800
; TELEFAX: (202) 833-8716
; TELEX: 248636 SSK
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-320-373-76

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Query Match          52.9%; Score 27; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 0;

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QY 1 GFGYKN 6
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Db 1 GFGYKN 6

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RESULT 3
US-08-973-563A-28
; Sequence 28, Application US/08973563A
; Patent No. 5885365
; GENERAL INFORMATION:
; APPLICANT: Oppenheim, Frank G.
; APPLICANT: Xu, Tao
; APPLICANT: Spacciapoli, Peter
; APPLICANT: Roberts, F. D.
; APPLICANT: Friden, Philip M.
; TITLE OF INVENTION: Anti-Fungal D-Amino Acid Histatin-Based
; TITLE OF INVENTION: Peptides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,563A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,273
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: PER95-02A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; INFORMATION FOR SEQ ID NO: 28:

```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..12
; OTHER INFORMATION: /note="At least one amino acid
; OTHER INFORMATION: must have a D configuration."
; US-08-973-563A-28

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```

Query Match          52.9%; Score 27; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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```

QY 2 FGYNKSF 9
   |||||
Db 5 FGYNKSF 12

```

```

RESULT 4
US-08-973-559-28
; Sequence 28, Application US/08973559
; Patent No. 5912230
; GENERAL INFORMATION:
; APPLICANT: OPPENHEIM, FRANK G.
; APPLICANT: XU, TAO
; APPLICANT: ROBERTS, F. D.
; APPLICANT: SPACCIAPOLI, PETER
; APPLICANT: FRIDEN, PHILIP M.
; TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial
; TITLE OF INVENTION: Histatin-Based Peptides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,559
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/481,888
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: PER95-01A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-973-559-28

```

```

Query Match          52.9%; Score 27; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY 2 FGYNKSF 9
 Db 5 FGYNKSF 12

RESULT 5

US-08-993-235-8
 ; Sequence 8, Application US/08993235
 ; Patent No. 6084064
 ; GENERAL INFORMATION:
 ; APPLICANT: OPPENHEIM, FRANK G.
 ; APPLICANT: ROBERTS, F. DONALD
 ; APPLICANT: XU, TAO
 ; APPLICANT: SPACCIAPOLI, PETER
 ; TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES
 ; FILE REFERENCE: 50032/002001
 ; CURRENT APPLICATION NUMBER: US/08/993,235
 ; CURRENT FILING DATE: 1997-12-18
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 8
 ; LENGTH: 12
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-08-993-235-8

Query Match 52.9%; Score 27; DB 3; Length 12;
 Best Local Similarity 62.5%; Pred. No. 78;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FGYNKSF 9
 Db 5 FGYNKSF 12

RESULT 6

US-09-226-666-4
 ; Sequence 4, Application US/09226666A
 ; Patent No. 6528488
 ; GENERAL INFORMATION:
 ; APPLICANT: Spacciapoli, Peter
 ; APPLICANT: Rothstein, David M.
 ; APPLICANT: Friden, Philip M.
 ; TITLE OF INVENTION: METHOD FOR TREATING CYSTIC FIBROSIS
 ; FILE REFERENCE: 50032/007001
 ; CURRENT APPLICATION NUMBER: US/09/226,666A
 ; CURRENT FILING DATE: 1999-01-08
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 12
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Derived from Homo sapiens
 US-09-226-666-4

Query Match 52.9%; Score 27; DB 4; Length 12;
 Best Local Similarity 62.5%; Pred. No. 78;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FGYNKSF 9
 Db 5 FGYNKSF 12

RESULT 7

US-08-993-235-8
 ; Sequence 8, Application US/08993235
 ; Patent No. 6531573
 ; GENERAL INFORMATION:
 ; APPLICANT: OPPENHEIM, FRANK G.

APPLICANT: ROBERTS, F. DONALD
 APPLICANT: XU, TAO
 APPLICANT: SPACCIAPOLI, PETER
 TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES
 FILE REFERENCE: 50032/002001
 CURRENT APPLICATION NUMBER: US/08/993,235
 CURRENT FILING DATE: 1997-12-18
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 8
 LENGTH: 12
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-08-993-235-8

Query Match 52.9%; Score 27; DB 4; Length 12;
 Best Local Similarity 62.5%; Pred. No. 78;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FGYNKSF 9
 Db 5 FGYNKSF 12

RESULT 8

US-09-613-182-2
 ; Sequence 2, Application US/09613182
 ; Patent No. 6294653
 ; GENERAL INFORMATION:
 ; APPLICANT: Mayfield, Stephen
 ; TITLE OF INVENTION: RNA BINDING PROTEIN AND BINDING SITE USEFUL FOR
 ; FILE REFERENCE: SCR2177S
 ; CURRENT APPLICATION NUMBER: US/09/613,182
 ; CURRENT FILING DATE: 2000-07-10
 ; PRIOR APPLICATION NUMBER: 09/341,550
 ; PRIOR FILING DATE: 1999-07-13
 ; PRIOR APPLICATION NUMBER: PCT/US98/00840
 ; PRIOR FILING DATE: 1998-01-16
 ; PRIOR APPLICATION NUMBER: 60/035,955
 ; PRIOR FILING DATE: 1997-01-17
 ; PRIOR APPLICATION NUMBER: 60/069,400
 ; PRIOR FILING DATE: 1997-12-12
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 14
 ; TYPE: PRT
 ; ORGANISM: Chlamydomonas reinhardtii
 US-09-613-182-2

Query Match 52.9%; Score 27; DB 3; Length 14;
 Best Local Similarity 62.5%; Pred. No. 91;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYNKSF 8
 Db 1 GFGYNKSF 8

RESULT 9

US-09-649-063-15
 ; Sequence 15, Application US/09649063
 ; Patent No. 6600022
 ; GENERAL INFORMATION:
 ; APPLICANT: TORIGOE, Kakuji
 ; APPLICANT: USHIO, Shimpel
 ; APPLICANT: KUNIKATA, Toshio
 ; APPLICANT: KURIMOTO, Masashi
 ; TITLE OF INVENTION: INTERLEUKIN-18 RECEPTOR PROTEINS
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/649,063
FILING DATE: 29-Aug-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,140
FILING DATE: <Unknown>
APPLICATION NUMBER: JP 52,526/1997
FILING DATE: 21-FEB-1997
APPLICATION NUMBER: JP 163,490/1997
FILING DATE: 6-JUN-1997
APPLICATION NUMBER: JP 215,490/1997
FILING DATE: 28-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOE-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-649-063-15
Query Match 49.0%; Score 25; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.se+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 GFGY 4
DB 7 GFGY 10
RESULT 10
US-09-150-621-60
Sequence 60, Application US/09150621
GENERAL INFORMATION:
APPLICANT: BAB, ITAI
APPLICANT: GAZIT, DAN
APPLICANT: YU-CHEN, CHEN
APPLICANT: MUHLRAD, ANDRAS
APPLICANT: SHTEYER, ARIE
APPLICANT: CHOREV, MICHAEL
TITLE OF INVENTION: SYNTHETIC PEPTIDES AND PSEUDOPEPTIDES HAVING OSTEOGENIC
TITLE OF INVENTION: ACTIVITY AND PHARMACEUTICAL COMPOSITIONS CONTAINING THE
TITLE OF INVENTION: SAME
FILE REFERENCE: 331949-140798
CURRENT APPLICATION NUMBER: US/09/150,621
CURRENT FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: PCT/IL97/00087
PRIOR FILING DATE: 1997-03-10
PRIOR APPLICATION NUMBER: 117426
PRIOR FILING DATE: 1996-03-10
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 60
LENGTH: 14

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
US-09-150-621-60

Query Match 49.0%; Score 25; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 GFGY 4
DB 2 GFGY 5

RESULT 11
US-08-973-563A-25
Sequence 25, Application US/08973563A
Patent No. 5885965
GENERAL INFORMATION:
APPLICANT: Oppenheim, Frank G.
APPLICANT: Xu, Tao
APPLICANT: Spacciapoli, Peter
APPLICANT: Roberts, P. D.
APPLICANT: Fritzen, Philip M.
TITLE OF INVENTION: Anti-Fungal D-Amino Acid Histatin-Based
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,563A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,273
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: PER95-02A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 1..12
OTHER INFORMATION: /note="At least one amino acid
OTHER INFORMATION: must have a D configuration."
US-08-973-563A-25

Query Match 48.0%; Score 24.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2 FGYNKSF 9
|||
Db 5 FGYNKSF 11

RESULT 12
US-08-973-563A-27
; Sequence 27, Application US/08973563A
; Patent No. 5885965
; GENERAL INFORMATION:
; APPLICANT: Oppenheim, Frank G.
; APPLICANT: Xu, Tao
; APPLICANT: Spacciapoli, Peter
; APPLICANT: Roberts, F. D.
; APPLICANT: Friden, Philip M.
; TITLE OF INVENTION: Anti-Fungal D-Amino Acid Histatin-Based
; TITLE OF INVENTION: Peptides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,563A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,273
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: PER95-02A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..12
; OTHER INFORMATION: /note="At least one amino acid
; OTHER INFORMATION: must have a D configuration."
US-08-973-563A-27

Query Match 48.0%; Score 24.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2 FGYNKSF 9
|||
Db 5 FGYNKSF 11

RESULT 13
US-08-973-559-25
; Sequence 25, Application US/08973559
; Patent No. 5912230
; GENERAL INFORMATION:
; APPLICANT: OPPENHEIM, FRANK G.

APPLICANT: XU, TAO
APPLICANT: ROBERTS, F. D.
APPLICANT: SPACCIAPOLI, PETER
APPLICANT: FRIDEN, PHILIP M.
TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial
TITLE OF INVENTION: Histatin-Based Peptides
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,559
FILING DATE: 07-JUN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,888
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: PER95-01A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-973-559-25

Query Match 48.0%; Score 24.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2 FGYNKSF 9
|||
Db 5 FGYNKSF 11

RESULT 14
US-08-973-559-27
; Sequence 27, Application US/08973559
; Patent No. 5912230
; GENERAL INFORMATION:
; APPLICANT: OPPENHEIM, FRANK G.
; APPLICANT: XU, TAO
; APPLICANT: ROBERTS, F. D.
; APPLICANT: SPACCIAPOLI, PETER
; APPLICANT: FRIDEN, PHILIP M.
; TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial
; TITLE OF INVENTION: Histatin-Based Peptides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973.559
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/481,888
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brock, David E.
; REGISTRATION NUMBER: 22,592
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-973-559-27

```

```

Query Match      48.0%; Score 24.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```

```

Qy      2 FGYNKSF 9
      |||||
      5 FGYNK-KF 11

```

```

RESULT 15
US-08-993-235-5
; Sequence 5, Application US/08993235
; Patent No. 6084064
; GENERAL INFORMATION:
; APPLICANT: OPPENHEIM, FRANK G.
; APPLICANT: ROBERTS, F. DONALD
; APPLICANT: XU, TAO
; APPLICANT: SPACCIAPOLI, PETER
; TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES
; FILE REFERENCE: 50032/002001
; CURRENT APPLICATION NUMBER: US/08/993.235
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-993-235-5

```

```

Query Match      48.0%; Score 24.5; DB 3; Length 12;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```

```

Qy      2 FGYNKSF 9
      |||||
      5 FGYNK-KF 11

```

```

RESULT 16
US-08-993-235-7
; Sequence 7, Application US/08993235
; Patent No. 6084064
; GENERAL INFORMATION:
; APPLICANT: OPPENHEIM, FRANK G.
; APPLICANT: ROBERTS, F. DONALD
; APPLICANT: XU, TAO

```

```

; APPLICANT: SPACCIAPOLI, PETER
; TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES
; FILE REFERENCE: 50032/002001
; CURRENT APPLICATION NUMBER: US/08/993.235
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-993-235-7

```

```

Query Match      48.0%; Score 24.5; DB 3; Length 12;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```

```

Qy      2 FGYNKSF 9
      |||||
      5 FGYNK-KF 11

```

```

RESULT 17
US-08-993-235-5
; Sequence 5, Application US/08993235
; Patent No. 6531573
; GENERAL INFORMATION:
; APPLICANT: OPPENHEIM, FRANK G.
; APPLICANT: ROBERTS, F. DONALD
; APPLICANT: XU, TAO
; APPLICANT: SPACCIAPOLI, PETER
; TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES
; FILE REFERENCE: 50032/002001
; CURRENT APPLICATION NUMBER: US/08/993.235
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-993-235-5

```

```

Query Match      48.0%; Score 24.5; DB 4; Length 12;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```

```

Qy      2 FGYNKSF 9
      |||||
      5 FGYNK-KF 11

```

```

RESULT 18
US-08-993-235-7
; Sequence 7, Application US/08993235
; Patent No. 6531573
; GENERAL INFORMATION:
; APPLICANT: OPPENHEIM, FRANK G.
; APPLICANT: ROBERTS, F. DONALD
; APPLICANT: XU, TAO
; APPLICANT: SPACCIAPOLI, PETER
; TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES
; FILE REFERENCE: 50032/002001
; CURRENT APPLICATION NUMBER: US/08/993.235
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-993-235-7

```

Query Match 48.0%; Score 24.5; DB 4; Length 12;
 Best Local Similarity 75.0%; Pred. No. 2.2e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 QY 2 FGYNKSF 9
 Db 5 FGYNK-KF 11

RESULT 19
 US-09-417-608A-86
 ; Sequence 86; Application US/09417608A
 ; Patent No. 6666164
 ; GENERAL INFORMATION:
 ; APPLICANT: Olsen, Arne
 ; APPLICANT: Roggen, Erwin
 ; APPLICANT: Ernst, Steffen
 ; TITLE OF INVENTION: Low Allergenic Protein Variants
 ; FILE REFERENCE: 5676.200-US
 ; CURRENT APPLICATION NUMBER: US/09/417,608A
 ; NUMBER OF SEQ ID NOS: 101
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 86
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 US-09-417-608A-86

Query Match 47.1%; Score 24; DB 4; Length 9;
 Best Local Similarity 66.7%; Pred. No. 3e+05;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 YKNSKF 9
 Db 3 FSNKSF 8

RESULT 20
 5217869-104
 ; Patent No. 5217869
 ; APPLICANT: KAUFAR, LAWRENCE M.
 ; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
 ; REAGENTS
 ; NUMBER OF SEQUENCES: 121
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/255,906
 ; FILING DATE: 11-OCT-1988
 ; SEQ ID NO:104;
 ; LENGTH: 9
 5217869-104

Query Match 47.1%; Score 24; DB 6; Length 9;
 Best Local Similarity 62.5%; Pred. No. 3e+05;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GFGYKSK 8
 Db 1 GFGYKSK 8

RESULT 21
 US-08-135-319A-8
 ; Sequence 8; Application US/08135319A
 ; Patent No. 6528487
 ; GENERAL INFORMATION:
 ; APPLICANT: Heavner, George A.
 ; APPLICANT: McEwen, Roger P.
 ; APPLICANT: Geny, Jian-Guo
 ; TITLE OF INVENTION: Peptide Inhibitors of Inflammation Mediated by Selectins
 ; FILE REFERENCE: CTC 102 CON

CURRENT APPLICATION NUMBER: US/06/135,319A
 ; CURRENT FILING DATE: 1993-10-12
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic inhibitory peptide
 US-08-135-319A-8

Query Match 47.1%; Score 24; DB 4; Length 10;
 Best Local Similarity 80.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YKNSKF 8
 Db 1 YKNSKF 5

RESULT 22
 US-09-383-667-29
 ; Sequence 29; Application US/09383667
 ; Patent No. 6624295
 ; GENERAL INFORMATION:
 ; APPLICANT: Adams, Camelia W.
 ; APPLICANT: Devaux, Brigitte
 ; APPLICANT: Baton, Dan L.
 ; APPLICANT: Haas, Philip E.
 ; APPLICANT: Judice, J. Kevin
 ; APPLICANT: Kirchofer, Daniel
 ; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
 ; FILE REFERENCE: P1661R2
 ; CURRENT APPLICATION NUMBER: US/09/383,667
 ; CURRENT FILING DATE: 1999-08-26
 ; EARLIER APPLICATION NUMBER: US 60/098,233
 ; EARLIER FILING DATE: 1998-08-28
 ; EARLIER APPLICATION NUMBER: US 60/122,767
 ; EARLIER FILING DATE: 1999-03-03
 ; NUMBER OF SEQ ID NOS: 32
 ; SEQ ID NO 29
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-383-667-29

Query Match 47.1%; Score 24; DB 4; Length 11;
 Best Local Similarity 80.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYK 5
 Db 2 GFGYK 6

RESULT 23
 US-09-347-926-9
 ; Sequence 9; Application US/09347926
 ; Patent No. 6440386
 ; GENERAL INFORMATION:
 ; APPLICANT: LEUNG, SHUI-ON
 ; TITLE OF INVENTION: STABILIZED RADIOPHOSPHATE-LABELLED PROTEINS
 ; FILE REFERENCE: 018733/0936
 ; CURRENT APPLICATION NUMBER: US/09/347,926
 ; CURRENT FILING DATE: 1999-07-06
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 9
 ; LENGTH: 12
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-347-926-9

Query Match 47.1% Score 24; DB 4; Length 12;
Best Local Similarity 66.7%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKN 6
| | | |
DB 4 GSGYEN 9

RESULT 24

5217869-103
Patent No. 5217869

APPLICANT: KATVAR, LAWRENCE M.
TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC

REAGENTS

NUMBER OF SEQUENCES: 121

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/255,906

FILING DATE: 11-OCT-1988

SEQ ID NO: 103;
LENGTH: 9
5217869-103

Query Match 46.1% Score 23.5; DB 6; Length 9;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 3 GYKSKF 9
| | | |
DB 1 GY-NSKF 6

RESULT 25

US-08-215-805A-3

Sequence 3, Application US/08215805A

Patent No. 5559008

GENERAL INFORMATION:

APPLICANT: Chang, Yung-Fu

TITLE OF INVENTION: LEUKOTOXIN GENE FROM PASTURELLA

NUMBER OF SEQUENCES: 84

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nixon, Hargrave, Devans & Doyle

STREET: Clinton Square, P.O. Box 1051

CITY: Rochester

STATE: New York

COUNTRY: USA

ZIP: 14603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/215,805A

FILING DATE: 22-MAR-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Timian, Susan J.

REGISTRATION NUMBER: 34,103

REFERENCE/DOCKET NUMBER: 19603/61 (D-1329A)

TELEPHONE: (716) 263-1636

TELEFAX: (716) 263-1600

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: Pasteurella suis

STRAIN: 5943

IMMEDIATE SOURCE:

LIBRARY: P. suis DNA in Bacteriophage lambda-daah

CLONE: (lambda)yc33-37

US-08-215-805A-3

Query Match 45.1% Score 23; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 YKSKF 9
| | | |
DB 1 FKSKF 6

RESULT 26

US-08-215-805A-41

Sequence 41, Application US/08215805A

Patent No. 5559008

GENERAL INFORMATION:

APPLICANT: Chang, Yung-Fu

TITLE OF INVENTION: LEUKOTOXIN GENE FROM PASTURELLA

NUMBER OF SEQUENCES: 84

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nixon, Hargrave, Devans & Doyle

STREET: Clinton Square, P.O. Box 1051

CITY: Rochester

STATE: New York

COUNTRY: USA

ZIP: 14603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/215,805A

FILING DATE: 22-MAR-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Timian, Susan J.

REGISTRATION NUMBER: 34,103

REFERENCE/DOCKET NUMBER: 19603/61 (D-1329A)

TELEPHONE: (716) 263-1636

TELEFAX: (716) 263-1600

INFORMATION FOR SEQ ID NO: 41:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: Actinobacillus pleuropneumoniae

US-08-215-805A-41

Query Match 45.1% Score 23; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 YKSKF 9
| | | |
DB 1 FKSKF 6

RESULT 27

US-08-630-915A-63

Sequence 63, Application US/08630915A

Patent No. 6309820

GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFMAN, No. 6309820h
APPLICANT: KAY, Brian K.
APPLICANT: FOMLERS, Dana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/630, 915A
APPLICATION NUMBER: US/08/630, 915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18, 872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-630-915A-63

Query Match 45.1%; Score 23; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKN 6
DB 1 GDGYKN 6

RESULT 28
US-09-638-203-6
Sequence 6, Application US/09638203
Patent No. 6602501
GENERAL INFORMATION:
APPLICANT: Daniel E.H. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Aya Jakobovits
APPLICANT: Arthur B. Raitano
TITLE OF INVENTION: NOVEL C-TYPE LECTIN TRANSMEMBRANE
TITLE OF INVENTION: ANTIGEN EXPRESSED IN HUMAN PROSTATE CANCER AND USES THEREOF
FILE REFERENCE: 129,20USU1
CURRENT APPLICATION NUMBER: US/09/638,203
CURRENT FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/148,935
PRIOR FILING DATE: 1999-08-12
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 9
TYPE: PRT

ORGANISM: Homo Sapiens
US-09-638-203-6

Query Match 45.1%; Score 23; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKN 7
DB 3 GFTYKTA 9

RESULT 29
US-09-638-203-28
Sequence 28, Application US/09638203
Patent No. 6602501
GENERAL INFORMATION:
APPLICANT: Daniel E.H. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Aya Jakobovits
APPLICANT: Arthur B. Raitano
TITLE OF INVENTION: NOVEL C-TYPE LECTIN TRANSMEMBRANE
TITLE OF INVENTION: ANTIGEN EXPRESSED IN HUMAN PROSTATE CANCER AND USES THEREOF
FILE REFERENCE: 129,20USU1
CURRENT APPLICATION NUMBER: US/09/638,203
CURRENT FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/148,935
PRIOR FILING DATE: 1999-08-12
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 9
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-638-203-28

Query Match 45.1%; Score 23; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKN 7
DB 3 GFTYKTA 9

RESULT 30
5217869-115
Patent No. 5217869
APPLICANT: RAUVAR, LAWRENCE M.
TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
REAGENTS
NUMBER OF SEQUENCES: 121
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/255,906
FILING DATE: 11-OCT-1988
SEQ ID NO:115
LENGTH: 9
5217869-115

Query Match 45.1%; Score 23; DB 6; Length 9;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKN 7
DB 1 GFGKHT 7

RESULT 31
US-08-855-958-4
Sequence 4, Application US/08855958B
Patent No. 6143723
GENERAL INFORMATION:

APPLICANT: Ramalah, Abduri
TITLE OF INVENTION: PIGMENTARY AGENT
FILE REFERENCE: 3146-132213
CURRENT APPLICATION NUMBER: US/08/855,958B
CURRENT FILING DATE: 1997-05-14
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 11
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: bFGF fragment
FEATURE:
OTHER INFORMATION: cyclo peptide
US-08-855-958-4

Query Match 45.1%; Score 23; DB 3; Length 11;
Best Local Similarity 42.9%; Pred. No. 3.9e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 GYKSKF 9
DB 1 GYRSRY 7

RESULT 32
US-08-855-958-9
Sequence 9, Application US/08855958B
Patent No. 6143723
GENERAL INFORMATION:
APPLICANT: Ramalah, Abduri
TITLE OF INVENTION: PIGMENTARY AGENT
FILE REFERENCE: 3146-132213
CURRENT APPLICATION NUMBER: US/08/855,958B
CURRENT FILING DATE: 1997-05-14
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 11
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: bFGF fragment
FEATURE:
OTHER INFORMATION: cyclo peptide
US-08-855-958-9

Query Match 45.1%; Score 23; DB 3; Length 11;
Best Local Similarity 42.9%; Pred. No. 3.9e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 GYKSKF 9
DB 1 GYRSRY 7

RESULT 33
US-09-407-687-28
Sequence 28, Application US/09407687
Patent No. 6548634
GENERAL INFORMATION:
APPLICANT: Ballinger, Marcus
APPLICANT: Kavanaugh, Michael
TITLE OF INVENTION: Synthetic Peptides Having FGF Receptor
FILE REFERENCE: 1517.001
CURRENT APPLICATION NUMBER: US/09/407,687
CURRENT FILING DATE: 1999-09-28
EARLIER APPLICATION NUMBER: 60/102,667
EARLIER FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 28
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic peptide
US-09-407-687-28

Query Match 45.1%; Score 23; DB 4; Length 12;
Best Local Similarity 66.7%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 YKSKF 9
DB 2 YENSPF 7

RESULT 34
US-09-254-733-50
Sequence 50, Application US/09254733
Patent No. 6277596
GENERAL INFORMATION:
APPLICANT: MATANABE, MANABU
APPLICANT: MORIYA, TATSUKI
APPLICANT: KOYAGI, KAORI
APPLICANT: SUMIDA, NAOMI
APPLICANT: MURAKAMI, TAKESHI
TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULASE cbl1 GENES ORIGINATING
TITLE OF INVENTION: IN TRICHODERMA VIRIDE AND SYSTEM FOR MASS-PRODUCING
FILE REFERENCE: 99-0266*/LC(WMC)/00144
CURRENT APPLICATION NUMBER: US/09/254,733
CURRENT FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 50
LENGTH: 14
TYPE: PRT
ORGANISM: TRICHODERMA VIRIDE MC300-1
US-09-254-733-50

Query Match 45.1%; Score 23; DB 3; Length 14;
Best Local Similarity 44.4%; Pred. No. 4.9e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GFGYKSKF 9
DB 6 GTGFNNGYF 14

RESULT 35
US-08-310-429A-14
Sequence 14, Application US/08310429A
Patent No. 5695935
GENERAL INFORMATION:
APPLICANT: Page, David C.
APPLICANT: Reijo, Renee
TITLE OF INVENTION: DAZ: A GENE ASSOCIATED WITH AZOOSPERMIA
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/310,429A

FILING DATE: 22-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH194-07
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-9540
TELEFAX: (617) 861-6240
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-310-429A-14

Query Match 43.1%; Score 22; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05; 1; Indels 0; Gaps 0;
Matches 3; Conservative 2; Mismatches 1;

Qy 1 GFGYKN 6
Db 2 GYGFTN 7

RESULT 36
US-08-690-734A-13
Sequence 13, Application US/08690734A
Patent No. 5871920
GENERAL INFORMATION:
APPLICANT: Page, David C.
TITLE OF INVENTION: DAZ: A GENE ASSOCIATED WITH AZOOSPERMIA
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690.734A
FILING DATE: 31-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,429
FILING DATE: 22-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH194-07A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-690-734A-13

Query Match 43.1%; Score 22; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GFGYKN 6
Db 2 GYGFTN 7

RESULT 37
US-08-031-538-30
Sequence 30, Application US/08031538
Patent No. 5968817
GENERAL INFORMATION:
APPLICANT: Sutcliffe, J Gregor
APPLICANT: Erlander, Mark G
APPLICANT: Lovenberg, Timothy W
TITLE OF INVENTION: HUMAN SEROTONIN RECEPTORS, DNA ENCODING
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5968817th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/031,538
FILING DATE: 19930315
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSR5099P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2
OTHER INFORMATION: /note= "Xaa is either Leu or Ile"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: /note= "Xaa is either Leu or Ser"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: /note= "Xaa is either Leu or Phe"
US-08-031-538-30

Query Match 43.1%; Score 22; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GYKNS 7
Db 3 GYKNS 7

RESULT 38
US-08-742-185-13

```
; Sequence 13, Application US/08742185
; Patent No. 6020476
; GENERAL INFORMATION:
; APPLICANT: Page, David C.
; APPLICANT: Reijo, Renee
; APPLICANT: Saxena, Richa
; APPLICANT: Hawkins, Trevor
; APPLICANT: Reeve, Mary Pat
; TITLE OF INVENTION: DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,185
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/690,734
; FILING DATE: 31-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/310,429
; FILING DATE: 22-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WHI94-07A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO. 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-742-185-13

Query Match          43.1% Score 22; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGYK 6
Db 2 GYGFVN 7

RESULT 39
US-09-082-279B-919
; Sequence 919, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
```

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 919
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
; US-09-082-279B-919

Query Match          43.1% Score 22; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGY 4
Db 4 GYGY 7

RESULT 40
US-09-315-304B-919
; Sequence 919, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 919
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
; US-09-315-304B-919

Query Match          43.1% Score 22; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGY 4
Db 4 GYGY 7

RESULT 41
US-09-834-784-919
; Sequence 919, Application US/09834784
; Patent No. 6562787
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/834,784
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
```


SEQ ID NO 919
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-834-784-919

Query Match
Best Local Similarity 43.1%; Score 22; DB 4; Length 8;
Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGY 4
Db 4 GYGY 7

RESULT 42
US-09-515-965A-919
Sequence 919, Application US/09515965A
Patent No. 6623741
GENERAL INFORMATION:
APPLICANT: Antczak, J.
APPLICANT: Delmedico, M.
APPLICANT: Erickson, J.
APPLICANT: Lambert, D.
APPLICANT: Sista, P.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
FILE REFERENCE: 7872-073
CURRENT APPLICATION NUMBER: US/09/515,965A
CURRENT FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1994
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 919
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-515-965A-919

Query Match
Best Local Similarity 43.1%; Score 22; DB 4; Length 8;
Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGY 4
Db 4 GYGY 7

RESULT 43
US-09-350-641C-919
Sequence 919, Application US/09350641C
Patent No. 6656906
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Mernitka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
FILE REFERENCE: 7872-067
CURRENT APPLICATION NUMBER: US/09/350,641C
CURRENT FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279

PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 919
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-350-641C-919

Query Match
Best Local Similarity 43.1%; Score 22; DB 4; Length 8;
Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGY 4
Db 4 GYGY 7

RESULT 44
US-08-467-580-31
Sequence 31, Application US/08467580B
Patent No. 6001809
GENERAL INFORMATION:
APPLICANT: Thorsett, Eugene D
APPLICANT: Yednock, Theodore A
APPLICANT: Pleiss, Michael A
TITLE OF INVENTION: Inhibitors of Leukocyte Adhesion
FILE REFERENCE: 123-US-C1P1
CURRENT APPLICATION NUMBER: US/08/467,580B
CURRENT FILING DATE: 1995-06-06
EARLIER APPLICATION NUMBER: 08/273,055
EARLIER FILING DATE: 1994-07-11
NUMBER OF SEQ ID NOS: 163
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 31
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide
OTHER INFORMATION: derived from first domain of VCAM-1
US-08-467-580-31

Query Match
Best Local Similarity 43.1%; Score 22; DB 3; Length 10;
Pred. No. 5.4e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKNS 7
Db 2 GFGYKNS 8

RESULT 45
US-08-990-015-7
Sequence 7, Application US/08990015A
Patent No. 6093701
GENERAL INFORMATION:
APPLICANT: Budker, Vladimír
APPLICANT: Hagstrom, James E.
APPLICANT: Sebestyen, Magdolna G.
APPLICANT: Wolff, John A.
TITLE OF INVENTION: A METHOD FOR COVALENT ATTACHMENT OF COMPOUNDS TO GENES
FILE REFERENCE: Covalent Attachment to Genes
CURRENT APPLICATION NUMBER: US/08/990,015A
CURRENT FILING DATE: 1997-12-12
EARLIER APPLICATION NUMBER: 60/050842
EARLIER FILING DATE: 1997-05-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 10

TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE: Description of Artificial Sequence: CONTAINS
OTHER INFORMATION: SEQUENCES FROM THE SV40 GENOME
US-08-990-015-7

Query Match 43.1%; Score 22; DB 3; Length 10;
Best Local Similarity 66.7%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 GYKNSK 8
|||
Db 2 GYKXKK 7

Search completed: August 30, 2004, 10:57:12
Job time : 4.55743 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2004, 10:39:14 ; Search time 13.4088 Seconds
(without alignments)
189.646 Million cell updates/sec

Title: US-09-720-469A-3
Perfect score: 51
Sequence: 1 GFGYKNSKF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 309569

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	9	3	AA69923 Human cyc
2	39	76.5	11	3	AA69924 Human cyc
3	30	58.8	12	5	ABG7066 Human pro
4	30	58.8	13	7	ADD44040 CP62 pep
5	30	58.8	13	7	ADD44091 CP62 pep
6	28	54.9	8	2	AA72924 Yeast PPI
7	28	54.9	8	2	AA72880 Yeast PPI
8	27	52.9	9	2	AAW33943 Betal-adr
9	27	52.9	10	5	AB88264 BAK prote
10	27	52.9	12	2	AAW19418 Anti-fung
11	27	52.9	12	2	AAW19464 Anti-fung
12	27	52.9	12	3	AAW25144 Antibacte
13	27	52.9	14	2	AAW1978 Histatin-
14	27	52.9	14	2	AAW33942 Betal-adr
15	27	52.9	14	2	AAW68100 Chlamydom
16	26	51.0	11	2	AAW16616 Phosphoin
17	26	51.0	12	5	AAO22420 Protease
18	26	51.0	14	4	AAW97164 Human pep
19	26	51.0	14	4	AAW99539 Vaccine r
20	26	51.0	14	7	ABD71196 Human mod
21	25	49.0	9	4	AAW99439 Vaccine r
22	25	49.0	9	4	AAW99577 Vaccine r
23	25	49.0	10	2	AAW28520 Human Her
24	25	49.0	10	2	AAW63824 Human Mab
25	25	49.0	10	4	AB46262 HPV type

26	25	49.0	10	6	ABR91208 P. papara
27	25	49.0	12	4	ABR81464 Synthetic
28	25	49.0	12	4	ABR81463 Synthetic
29	25	49.0	12	5	ABR74314 Simple na
30	25	49.0	12	5	AAE28582 Desmodium
31	25	49.0	13	2	AAW94978 MHC bindi
32	25	49.0	13	3	AAW13279 Caenorhab
33	25	49.0	13	7	ADD44065 CP62 pep
34	25	49.0	13	7	ADD44039 CP62 pep
35	25	49.0	14	2	ADCT3226 Retro ost
36	25	49.0	14	4	AAU68422 Human Bre
37	25	49.0	14	4	AAU25297 Schizophr
38	25	49.0	14	4	AAU15641 Human API
39	25	49.0	14	4	ABR52298 Human API
40	25	49.0	14	5	AAE25488 CAP1-19 t
41	25	49.0	14	5	ABJ15069 Human 125
42	25	49.0	14	5	ABG67720 Human ADP
43	25	49.0	14	6	ABY11220 P. papara
44	25	49.0	14	6	ABR59105 Alzheimer
45	25	49.0	14	6	ADA23853 Alzheimer

ALIGNMENTS

RESULT 1
ID AA69923 standard; peptide; 9 AA.
AC AA69923;
DT 11-APR-2000 (first entry)
XX Human cyclophilin B peptide fragment #3.
DE Human cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
XX Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX Homo sapiens.
OS MO9967288-AA.
XX 29-DEC-1999.
PD 24-JUN-1999; 99MO-JP003360.
XX 25-JUN-1998; 98JP-00178449.
PR (SUMO) SUMITOMO PHARM CO LTD.
PA (ITOH) ITOH K.
XX Itoh K, Gomi S,
XX WPI; 2000-116932/10.
PT Tumour antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX Claim 4; Page 50; 64pp; Japanese.
PS This sequence represents a cyclophilin B peptide of the invention. The
XX peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX Sequence 9 AA;
SQ
Query Match 100.0%; Score 51; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 GFGYKNSKF 9
|||||||

Db 1 GFGRKSKF 9

RESULT 2

AA69924

ID AA69924 standard; peptide: 11 AA.

AC AA69924;

DT 11-APR-2000 (first entry)

DE Human cyclophilin B peptide fragment #4.

KM Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;

KM HLA antigen; diagnosis; tumour; therapy.

OS Homo sapiens.

OS Homo sapiens.

PN WO967288-A1.

PD 29-DEC-1999.

PF 24-JUN-1999; 99WO-JP003360.

PR 25-JUN-1998; 98JP-00178449.

PA (SUMU) SUMITOMO PHARM CO LTD.

PI (ITOH) ITOH K.

PI Itoh K, Gomi S;

DR WPI; 2000-116932/10.

PT Tumour antigen peptides derived from cyclophilin B for treatment and

PT diagnosis of tumors.

PS Claim 4; Page 50; 64pp; Japanese.

CC This sequence represents a cyclophilin B peptide of the invention. The

CC peptides are tumour antigen peptides derived from cyclophilin B, that

CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The

CC peptides are used for the treatment and diagnosis of tumours

CC Sequence 11 AA;

OY 3 GFGRKSKF 9

Db 1 GFGRKSKF 7

ID ABG70966 standard; peptide: 12 AA.

AC ABG70966;

DT 04-DEC-2002 (first entry)

DE Human protein kinase Cbeta1 peptide.

KM Human; radiotherapeutic agent precursor; targeting peptide; tumour;

KM phosphorylation peptide; linker; Src homology region 2 domain; SH_2;

KM infectious lesion; breast; colon; rectum; prostate; ovary; testes;

KM pathological lesion; chest; abdomen; pelvis; skin; cardiovascular lesion;

KM myocardial infarct; atherosclerotic plaque; clot; thrombosis;

KM pulmonary embolism; inflammatory lesion; hyperplasia;

KM protein kinase Cbeta1.

OS Homo sapiens.

XX US6440386-B1.

XX 27-AUG-2002.

XX 06-JUL-1999; 99US-00347926.

XX 06-JUL-1998; 98US-0091736P.

XX (IMMUNO-) IMMUNOMEDICS INC.

XX Leung S;

DR WPI; 2002-722167/78.

PT Radioactive agent precursor, useful in manufacture of in vivo

PT radiotherapeutic agents, comprises protein containing targeting peptide,

PT phosphorylation peptide, linker and Src homology region 2 domain.

PS Disclosure; Col 7; 13pp; English.

CC The present invention relates to a new radiotherapeutic agent precursor

CC comprising a protein containing a targeting peptide, a phosphorylation

CC peptide, a linker and Src homology region 2 domain (SH_2). The invention

CC is useful for preparing radiotherapeutic agents, useful for the treatment

CC of tumour and an infectious lesion. The lesions include infectious

CC lesions of breast, colon, rectum, prostate, ovary and testes;

CC cardiovascular lesions affecting chest, abdomen and pelvis; and skin; and

CC plaque, clot, thrombosis, pulmonary embolism, inflammatory lesions and

CC hyperplasia. The linker in the radiotherapeutic agent is long and fold

CC back on the phosphorylated substrate. Thus, the radiotherapeutic agent

CC exhibits improved stability in vivo, by avoiding the ready

CC phosphorylation, while maintaining the binding ability of the agent. The

CC present amino acid sequence represents a human peptide that contains an

CC SH_2 domain as described in the invention

XX Sequence 12 AA;

OY 1 GFGRKSKF 9

Db 4 GFGRKSKF 12

ID ADD44040 standard; peptide: 13 AA.

AC ADD44040;

DT 15-JAN-2004 (first entry)

DE CPG2 peptide #60 with potential human MHC class II binding activity.

KM bacterial enzyme; carboxypeptidase G2; CPG2; non-immunogenic;

KM immunogenic; T-cell epitope; MHC class II binding ligand;

KM immunostimulant; enzyme therapy; immune response;

KM gene directed enzyme prodng strategy; vaccine; enzyme; EC 3.4.17.11.

OS Pseudomonas sp. RS-16.

PN WO2003045426-A1.

PN 05-JUN-2003.

PF 27-NOV-2002; 2002WO-EP013351.

PR 29-NOV-2001; 2001EP-00128519.

PR 25-JAN-2002; 2002EP-00001778.
 PR 13-SEP-2002; 2002EP-00020634.
 PA (MERCK) MERCK PATENT GMBH.
 PI Hellendoorn K, Baker M, Williams S, Carr FU;
 DR WPI; 2003-513617/48.
 PR New modified bacterial enzyme carboxypeptidase G2 (CPG2) having
 PT substantially non-immunogenic or less immunogenic than any non-modified
 PT CPG2, useful for inducing an immune response in a human host.
 XX
 XX
 PS Claim 3; Page 13; 52pp; English.
 CC The invention relates to a novel modified bacterial enzyme
 CC carboxypeptidase G2 (CPG2). The modified enzyme can result in CPG2
 CC proteins that are substantially non-immunogenic or less immunogenic than
 CC any non-modified CPG2 having essentially the same biological specificity
 CC when used in vivo, and comprising specifically amino acid residues having
 CC alterations compared with the non-modified parochial enzyme. The
 CC alterations cause a reduction or an elimination of one or more of T-cell
 CC epitope sequences, which act in the parental enzyme as MHC class II
 CC binding ligands and stimulate T-cells. The modified CPG2 enzyme and the
 CC CPG2 proteins have immunostimulant activity and may be used in enzyme
 CC therapy. The modified CPG2 enzyme may be used to induce an immune
 CC response in a human host, or as a therapeutic entity such as the gene
 CC directed enzyme prodng strategy. The peptide is useful for the
 CC manufacture of a modified CPG2 enzyme having substantially no or less
 CC immunogenicity than any non-modified parental enzyme when used in vivo,
 CC and for vaccination of patients to reduce immunogenicity to CPG2 in vivo.
 CC This sequence represents a CPG2 enzyme peptide with potential human MHC
 CC class II binding activity of the invention.
 XX
 XX
 SQ Sequence 13 AA;
 Query Match 58.8%; Score 30; DB 7; Length 13;
 Best Local Similarity 62.5%; Pred. No. 1.1e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GFGYKNSK 8
 Db 2 GFGYHSDX 9
 RESULT 5
 ADD44091
 ID ADD44091 standard; peptide; 13 AA.
 AC ADD44091;
 XX
 DT 15-JAN-2004 (first entry)
 DE CPG2 peptide #11 with potential human MHC class II binding activity.
 XX
 XX bacterial enzyme; carboxypeptidase G2; CPG2; non-immunogenic;
 KW immunogenic; T-cell epitope; MHC class II binding ligand;
 KW immunostimulant; enzyme therapy; immune response;
 KW gene directed enzyme prodng strategy; vaccine; enzyme; EC 3.4.17.11.
 XX
 OS Pseudomonas sp. RS-16.
 XX
 PN WO2003045426-A1.
 PD 05-JUN-2003.
 XX
 PF 27-NOV-2002; 2002WO-EP013351.
 XX
 PR 29-NOV-2001; 2001EP-00128519.
 PR 25-JAN-2002; 2002EP-00001778.
 PR 13-SEP-2002; 2002EP-00020634.
 XX
 PA (MERCK) MERCK PATENT GMBH.

XX
 PI Hellendoorn K, Baker M, Williams S, Carr FU;
 DR WPI; 2003-513617/48.
 PR New modified bacterial enzyme carboxypeptidase G2 (CPG2) having
 PT substantially non-immunogenic or less immunogenic than any non-modified
 PT CPG2, useful for inducing an immune response in a human host.
 XX
 XX
 PS Claim 3; Page 13; 52pp; English.
 CC The invention relates to a novel modified bacterial enzyme
 CC carboxypeptidase G2 (CPG2). The modified enzyme can result in CPG2
 CC proteins that are substantially non-immunogenic or less immunogenic than
 CC any non-modified CPG2 having essentially the same biological specificity
 CC when used in vivo, and comprising specifically amino acid residues having
 CC alterations compared with the non-modified parochial enzyme. The
 CC alterations cause a reduction or an elimination of one or more of T-cell
 CC epitope sequences, which act in the parental enzyme as MHC class II
 CC binding ligands and stimulate T-cells. The modified CPG2 enzyme and the
 CC CPG2 proteins have immunostimulant activity and may be used in enzyme
 CC therapy. The modified CPG2 enzyme may be used to induce an immune
 CC response in a human host, or as a therapeutic entity such as the gene
 CC directed enzyme prodng strategy. The peptide is useful for the
 CC manufacture of a modified CPG2 enzyme having substantially no or less
 CC immunogenicity than any non-modified parental enzyme when used in vivo,
 CC and for vaccination of patients to reduce immunogenicity to CPG2 in vivo.
 CC This sequence represents a CPG2 enzyme peptide with potential human MHC
 CC class II binding activity of the invention.
 XX
 XX
 SQ Sequence 13 AA;
 Query Match 58.8%; Score 30; DB 7; Length 13;
 Best Local Similarity 62.5%; Pred. No. 1.1e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GFGYKNSK 8
 Db 5 GFGYHSDX 12
 RESULT 6
 AAR72924
 ID AAR72924 standard; peptide; 8 AA.
 AC AAR72924;
 XX
 DT 16-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 29-NOV-1995 (first entry)
 XX
 DE Yeast PPIase tryptic fragment 4.
 XX
 XX Escherichia coli; protein conformation; folding; acceleration;
 KW PPIase-alpha; peptidyl prolyl cis trans isomerase alpha; catalysis;
 KW isomerisation; prolyl peptide bond.
 XX
 OS Saccharomyces cerevisiae; strain AH22.
 XX
 PN EP647714-A1.
 PD 12-APR-1995.
 PF 19-JUL-1990; 94EP-00203612.
 XX
 PR 19-JUL-1989; 89JP-00184738.
 PR 06-OCT-1989; 89JP-00260244.
 PR 29-DEC-1989; 89JP-00344705.
 PR 19-JUL-1990; 90EP-00307914.
 XX
 PA (TOFU) TONEN CORP.
 XX
 PI Hayano T, Katou S, Maki N, Takahashi N, Suzuki M,

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XX DR WPI, 1995-140756/19.
XX CC
XX PT New E.coli peptidyl prolyl cis trans isomerase beta - used to accelerate
XX PT the folding of proteins, partic. for activation of inactive recombinant
XX PT proteins.
XX PS Example 2; Page 22; 85pp; English.
XX CC AAR2921-29 are tryptic fragments of a yeast PPIase (peptidyl prolyl cis
XX CC trans isomerase). The yeast PPIase has a single mol. wt. of about 17 kDa
XX CC and a single isoelectric point of about 6.2. The enzyme catalyzes the
XX CC isomerisation of prolyl peptide bonds in proteins and accelerates the
XX CC folding of the protein. The inventors are claiming a PPIase-beta.
XX CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to
XX CC correct PF field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated
XX CC on 16-OCT-2003 to standardise OS field)
XX SQ Sequence 8 AA;

Query Match          54.9%; Score 28; DB 2; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKNS 7
   |||||
Db 1 GFGYAGS 7

RESULT 7
AAR2880
ID AAR2880 standard; peptide; 8 AA.
XX AC
XX AA AAR2880;
XX DT 16-OCT-2003 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 29-NOV-1995 (first entry)
XX DE Yeast PPIase tryptic fragment 4.
XX KM Escherichia coli; protein conformation; folding; acceleration;
XX KM PPIase-alpha; peptidyl prolyl cis trans isomerase alpha; catalysis;
XX KM isomerisation; prolyl peptide bond.
XX OS Saccharomyces cerevisiae; strain AH22.
XX PN BP647713-A1.
XX PD 12-APR-1995.
XX PF 19-JUL-1990; 94EP-00203610.
XX PR 19-JUL-1989; 89JP-00184738.
XX PR 06-OCT-1989; 89JP-00260244.
XX PR 29-DEC-1989; 89JP-00344705.
XX PR 19-JUL-1990; 90EP-00307914.
XX PA (TOFU) TONEN CORP.
XX PI Hayano T, Katou S, Maki N, Takahashi N, Suzuki M;
XX WPI; 1995-140755/19.
XX DR
XX PT New E.coli peptidyl prolyl cis trans isomerase alpha - used to accelerate
XX PT the folding of proteins, partic. for activation of inactive recombinant
XX PT proteins.
XX PS Example 2; Page 22; 85pp; English.
XX CC AAR2897-85 are tryptic fragments of a yeast PPIase (peptidyl prolyl cis
XX CC trans isomerase). The yeast PPIase has a single mol. wt. of about 17 kDa
XX CC and a single isoelectric point of about 6.2. The enzyme catalyzes the

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CC CC isomerisation of prolyl peptide bonds in proteins and accelerates the
CC CC folding of the protein. The inventors are claiming the PPIase-alpha
CC CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to
CC CC correct PF field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated
CC CC on 16-OCT-2003 to standardise OS field)
XX SQ Sequence 8 AA;

Query Match          54.9%; Score 28; DB 2; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKNS 7
   |||||
Db 1 GFGYAGS 7

RESULT 8
AAM33943
ID AAM33943 standard; peptide; 9 AA.
XX AC
XX AA AAM33943;
XX DT 28-MAY-1998 (first entry)
XX DE Beta1-adrenergic receptor antagonist.
XX KM Antagonist; integral membrane protein; inhibitor; transmembrane domain;
XX KM therapy; psychotic disorder; Huntington's disease; Parkinson's disease;
XX KM post-myocardial infarction; HIV infection; cell proliferation disorder;
XX KM peptic ulcer; glaucoma; asthma; renal disease; autoimmune disease;
XX KM antibacterial; beta1-adrenergic receptor.
XX OS Homo sapiens.
XX PN WO9735881-A2.
XX PD 02-OCT-1997.
XX PF 26-MAR-1997; 97WO-CAN00203.
XX PR 27-MAR-1996; 96US-0014306P.
XX PR 25-JUN-1996; 96US-00670119.
XX PR 20-AUG-1996; 96US-0024240P.
XX PA (NGX/) NG G Y K.
XX PA (SEEM/) SEEMAN P.
XX PA (GEOR/) GEORGE S R.
XX PA (ODOM/) O'DOMD B F.
XX PI Ng GYK, Seeman P, George SR, Odowd BF;
XX WPI; 1997-489566/45.
XX DR
XX PT Inhibitor of integral membrane protein - used to treat e.g.
XX PT schizophrenia, hypertension, viral infection, cancer etc.
XX PS Claim 17; Page 94; 127pp; English.
XX CC This sequence is a beta1-adrenergic receptor antagonist, and is an
XX CC antagonist of the invention. The antagonists (A) are for inhibiting the
XX CC function of a prokaryotic or eukaryotic integral membrane protein (IMP)
XX CC having at least one transmembrane domain (TMD), comprises a peptide
XX CC including at least 4 consecutive amino acids (aa) from the sequence of
XX CC the TMD. (A) are used to treat or prevent disorders in mammals that
XX CC involve disturbances of IMP, and the same effect is achieved by inserting
XX CC a nucleic acid encoding (A) into the cells of the mammal. Specified
XX CC conditions that can be treated are schizophrenia, psychotic disorders,
XX CC Huntington's disease, Tourette's syndrome, hypertension, post-myocardial
XX CC infarction, tachyarrhythmia, human immunodeficiency virus infection,
XX CC AIDS, cell proliferation (cancer, psoriasis or hyperkeratosis), and drug
XX CC abuse. (A) can also be used to treat peptic ulcer, glaucoma, asthma,
XX CC renal disease, Parkinson's disease, congestive heart failure, migraine,

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CC depression, obesity, diabetic neuropathy/retinopathy, autoimmune
 CC diseases, graft rejection etc. (A) can be used as diuretics and
 CC antibacterials. (A) may also be used to determine function of orphan
 CC receptors and, when attached to a marker, for tissue imaging to
 CC localise/quantify specific receptors. The transgenic animals are used to
 CC test efficacy/toxicity of (A) and as models of diseases. (A) are very
 CC specific and selective, against the IMP from which they are derived, so
 CC should have few side effects
 CC
 XX Sequence 9 AA:

Query Match 52.9%; Score 27; DB 2; Length 9;
 Best Local Similarity 71.4%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GYKNSKF 9
 |||||
 Db 1 GYNSAF 7

RESULT 9
 ABB82364
 ID ABB82364 standard; peptide; 10 AA.

XX ABB82364;
 AC
 XX 08-JAN-2003 (first entry)
 DT
 XX
 DE BAK protein fragment.

XX BAK, MLL; cytosolic; neuroprotective; nootropic; cerebroprotective;
 KM apoptosis; human.

XX Homo sapiens.

OS WO200274908-A2.

PN 26-SEP-2002.

PD 04-MAR-2002; 2002WO-US006757.

PF 02-MAR-2001; 2001US-0273091P.

PR (MDS-PROTEOMICS INC.

PA McFadden G, Moran MF;

PI WPI; 2002-740855/80.

DR Identifying agents which may be potentially pro-apoptotic or anti-
 XX apoptotic for treating acute and chronic neurodegenerative disease,
 PT comprises determining the effect of the test agent on complexes of BAK
 PT and/or MLL proteins.
 XX
 PS Disclosure; Page 14; 83pp; English.

XX The invention relates to identifying agents which may be potentially pro-
 CC apoptotic or anti-apoptotic which involves determining the effect of a
 CC test agent on the complexes of BAK and/or MLL proteins. The methods are
 CC useful for identifying agents which may be potentially pro-apoptotic or
 CC anti-apoptotic and for identifying MLL-interacting polypeptides, and in
 CC conducting a target or drug discovery system. The methods are useful for
 CC identifying agents capable of inhibiting MLL activity or which can mimic
 CC the activity of MLL by inhibiting the activity of BAK and which are
 CC therefore anti-apoptotic agents. Agents identified by the method as
 CC involved in regulation of apoptosis may be used in the development of
 CC therapeutic agents and methods, and drug screening assays, and in
 CC increasing the sensitivity of cancer cells to chemotherapeutic treatment.
 CC Therapeutic applications of apoptosis manipulation include treatment of
 CC acute and chronic neurodegenerative diseases, e.g. stroke, Alzheimer's or
 CC Huntington's disease by drugs, and sensitization of cancer cells for drug
 CC /radiation-induced apoptosis by modulation of survival signals and vital
 CC transfer of apoptosis promoting genes. The present sequence represents a

CC BAK protein fragment
 XX
 SQ Sequence 10 AA;

Query Match 52.9%; Score 27; DB 5; Length 10;
 Best Local Similarity 80.0%; Pred. No. 3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGYK 5
 |||||
 Db 6 GFGYR 10

RESULT 10
 AAM19418
 ID AAM19418 standard; peptide; 12 AA.

XX AAM19418;

DT 05-SEP-1997 (first entry)

DE Anti-fungal and anti-bacterial histatin-based peptide 113-F4.5.12.

XX Candida albicans; periodontitis; caries; tooth decay; oral infection;
 KM vaginal infection; urethral infection; mucosal infection; ear infection;
 KM respiratory infection; skin infection; ophthalmic infection;
 KM bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;
 KM Clostridium histolyticum.

XX Synthetic.

OS Key Location/Qualifiers

FT Region 1. .12
 FT /note= "At least one amino acid must have a D-
 FT configuration"

XX WO9640768-A2.

PN 19-DEC-1996.

PD 07-JUN-1996; 96WO-US009374.

PF 07-JUN-1995; 95US-00481888.

PR (PERI-) PERIODONTIX INC.

PA (UYBO-) UNIV BOSTON.

PI Oppenheim FG, Xu T, Roberts PD, Spacciapoli P, Friden PM;

DR WPI; 1997-052232/05.
 XX Anti-fungal and anti-bacterial histatin-based peptide(s) - useful esp for
 PT treating Candidal infections, periodontitis and caries.
 PT
 XX Claim 2; Fig 1; 72pp; English.

XX The present sequence represents a specifically claimed peptide sequence,
 CC peptide 113-F4.5.12, where at least one amino acid is in the D-
 CC configuration. The peptide preferably is modified by an acetyl or
 CC carbamyl addition at the N-terminus and/or amidation at the C-terminus.
 CC The peptide, based on the naturally occurring histidine-rich human
 CC histatins, have anti-fungal and anti-bacterial activity and are useful in
 CC compositions for the treatment of oral, vaginal, urethral, mucosal,
 CC respiratory, skin, ear and ophthalmic fungal or bacterial infections. It
 CC is particularly effective against local and systemic Candida albicans
 CC infection, against oral bacterial diseases such as caries and
 CC periodontitis (by inhibiting e.g. Streptococcus mutans and Porphyromonas
 CC gingivalis) and against Clostridium histolyticum. The peptide has
 CC superior anti-fungal (especially anti-Candida) and anti-bacterial
 CC activity, particularly on a weight basis, compared to the longer,
 CC naturally occurring histatins. Peptides containing D-residues are also
 CC more resistant to degradation than L-amino acid versions

SQ Sequence 12 AA;

Query Match 52.9%; Score 27; DB 2; Length 12;
 Best Local Similarity 62.5%; Pred. No. 3.6e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FGYKSKPF 9
 DB 5 FGKRRKPF 12

RESULT 11

AAW19464 standard; peptide: 12 AA.

AAW19464;

05-SEP-1997 (first entry)

Anti-fungal and anti-bacterial D-amino acid peptide 113-F4.5.12.

Candida albicans; periodontitis; caries; tooth decay; oral infection;
 vaginal infection; urethral infection; mucosal infection; ear infection;
 respiratory infection; skin infection; ophthalmic infection;
 bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;
 Clostridium histolyticum.

Synthetic.

Key Location/Qualifiers
 1..12
 /note= "At least one amino acid must have D-configuration"

MO9640770-AZ.

19-DEC-1996.

07-JUN-1996; 96WO-US0009962.

07-JUN-1995; 95US-00485273.

(PERI-) PERIODONTIX INC.

(UYBO-) UNIV BOSTON.

Oppeheim FG, Xu T, Spacciapoli P, Roberts FD, Friden PM;
 WPI; 1997-052234/05.

Anti-fungal and anti-bacterial D-amino acid histatin and histatin-based
 peptide(s) - useful esp for treating Candidal infections, periodontitis
 and caries.

Claim 2; Fig 1; 63pp; English.

The present sequence represents a specifically claimed example of an anti-
 fungal and anti-bacterial D-amino acid histatin-based peptide 113-
 F4.5.12, where at least one amino acid in the peptide is in the D-
 configuration. The peptide is preferably modified by an acetyl or
 carbamyl addition at the N-terminus and/or amidation at the C-terminus.
 The novel D-amino acid-containing peptide, based on the naturally
 occurring histidine-rich human histatins, have anti-fungal and anti-
 bacterial activity and are useful in compositions for the treatment of
 oral, vaginal, urethral, mucosal, respiratory, skin, ear and ophthalmic
 fungal or bacterial infections. It is particularly effective against
 local and systemic Candida albicans infection, against oral bacterial
 diseases such as caries and periodontitis (by inhibiting e.g.
 Streptococcus mutans and Porphyromonas gingivalis) and against
 Clostridium histolyticum. The D-amino acid-containing peptide has
 superior anti-fungal (especially anti-candidal) and anti-bacterial
 activity, particularly on a weight basis, compared to the natural L-
 amino acid forms of histatins and histatin-based peptides. The presence
 of D-residues also makes the peptides more resistant to degradation than

CC corresponding L-amino acid versions

SQ Sequence 12 AA;

Query Match 52.9%; Score 27; DB 2; Length 12;
 Best Local Similarity 62.5%; Pred. No. 3.6e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FGYKSKPF 9
 DB 5 FGKRRKPF 12

RESULT 12

AAW25144 standard; peptide: 12 AA.

AAW25144;

27-AUG-1999 (first entry)

Anti-bacterial and antifungal peptide 5.

Anti-fungal; antibacterial; treatment; infection; candidal; ophthalmic;
 viral vaginal; urethral; mucosal; respiratory; skin; ear; oral.

Unidentified.

MO9911123-A1.

24-JUN-1999.

14-DEC-1998; 98WO-US026513.

18-DEC-1997; 97US-00993235.

(PERI-) PERIODONTIX INC.

(UYBO-) UNIV BOSTON.

Roberts FD, Spacciapoli P, Friden PM, Oppeheim FG, Xu T;

WPI; 1999-395161/33.

Antibacterial and antifungal peptides.

Disclosure, Page 8; 31pp; English.

This invention describes novel substantially pure antibacterial and
 antifungal peptides (A) containing between 13 and 20 amino acids, where
 the peptide has the amino acid sequence: R1-R2-R3-R4-R5-R6-R7-R8-R9-R10-
 R11-R12-R13-R14-R15-R16-R17-R18-R19-R20-R21-R22-R23; where: R1 is Asp or
 absent; R2 and R20 are Ser or absent; R3, R18, R19 and R21 are His or
 absent; R4 is Ala; R5, R6, R9, R12, R13, are Lys, Gln, Arg or another
 basic amino acid; R7, R8 and R15 are His, Tyr, Leu, another
 hydrophobic amino acid, or is absent; R10 is Tyr; R16 is Gln or absent;
 R17 is Lys or absent; R22 is Arg or absent; R23 is Gly or absent; where
 Gln cannot simultaneously occupy positions R5, R6, R12, and R13 of the
 amino acid sequence. (A) can be used to treat fungal or bacterial
 infection in a mammal. The peptides are particularly used to treat
 candidal infection, as well as bacterial and viral infections, especially
 vaginal, urethral, mucosal, respiratory, skin, ear, oral, or ophthalmic
 infections. The infections that can be treated include those caused by
 Candida albicans, Actinomyces actinomycetemcomitans, Actinomyces
 viscosus, Bacteroides forsythus, Bacteroides gracilis, Bacteroides
 ureolyticus, Campylobacter concisus, Campylobacter rectus, Campylobacter
 showae, Campylobacter sputorum, Capnocytophaga gingivalis, Capnocytophaga
 ochracea, Capnocytophaga sputigena, Clostridium histolyticum, Eikenella
 corrodens, Eubacterium nodatum, Fusobacterium nucleatum, Fusobacterium
 periodonticum, Peptostreptococcus nictros, Porphyromonas endodontalis,
 Porphyromonas gingivalis, Prevotella intermedia, Prevotella nigrescens,
 Propionibacterium acnes, Pseudomonas aeruginosa, and those caused by
 various Streptococcal and Streptococcal species. AAW25140-Y25149 are
 peptides used in the description of the invention

XQ Sequence 12 AA; 52.9%; Score 27; DB 2; Length 12;
Query Match Best Local Similarity 62.5%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 FGYNKSKF 9
|||
Db 5 FGYKXKFP 12

RESULT 13
AAB11978
ID AAB11978 standard, peptide; 12 AA.
AC AAB11978;
XX
DT 24-NOV-2000 (first entry)
DE Histatin-related peptide, P-113-P4.5.12.
KW Histatin-related peptide; cystic fibrosis; Pseudomonas aeruginosa;
antibiotic resistance; pulmonary infection; antibacterial; antibiotic.

OS Homo sapiens.
CS Synthetic.
PM WO200040204-AZ.
PD 13-JUL-2000.
PF 07-JAN-2000; 200OWO-US000480.
PR 08-JAN-1999; 99US-00226666.
PA (PERI-) PERIOCONTIX INC.
PI Spacciapoli P, Rothstein DM, Friden PM;
WP1: 2000-465852/40.

Treating cystic fibrosis and combating Pseudomonas and other pulmonary infections in a mammal comprises administering histatin or a fragment of it.

Claim 32; Page 19; 27pp; English.

The invention relates to treating cystic fibrosis via the administration of a histatin, a fragment of histatin, or a histatin-related peptide. The peptide that is administered contains between 8 and 20 amino acids and has the sequence: X1-X2-X3-X4-X5-X6-X7-X8-X9-X10-X11-X12-X13-X14-X15-X16-X17-X18-X19-X20-X21-X22-X23 where X1 is Asp or absent; X2 is Ser or absent; X3 is His or absent; X4 is Ala, His, Leu or absent; X5 is Lys, Gln, Arg, Orn, or another basic amino acid; X6 is Arg, Gln, Lys, or another basic amino acid; X7 is His, Phe, Tyr, Leu, or another hydrophobic amino acid; X8 is His, Phe, Tyr, Leu, or another hydrophobic amino acid; X9 is Gly, Lys, Arg, Ser, or a basic amino acid; X10 is Tyr, X11 is Lys, His, Phe, Leu, or another hydrophobic amino acid; X12 is Lys, Gln, Arg, Orn, or another basic amino acid; X13 is Lys, Gln, Arg, Orn, another basic amino acid, or absent; X14 is Phe or absent; X15 is His, Phe, Tyr, Leu, or another hydrophobic amino acid, or absent; X16 is Gln or absent; X17 is Lys or absent; X18 is His or absent; X19 is His or absent; X20 is Ser or absent; X21 is His or absent; X22 is Arg or absent; and X23 is Gly or absent. Optionally, the peptide may contain at least one modification selected from an N-terminal acyl addition, an N-terminal carboxy addition and a C-terminal amide addition. Histatin, histatin fragments and histatin-related peptides have activity against Pseudomonas aeruginosa. They may therefore be used to combat Pseudomonas infections and other pulmonary infections in cystic fibrosis patients. Such infections are often resistant to the antibiotics normally used to treat pulmonary infections. Sequences ABB11976-B11984 represent specifically claimed histatin-related peptides for use in the method of the invention

XX	Sequence	12 AA;
SQ		
	Query Match	52.9%; Score 27; DB 3; Length 12;
	Best Local Similarity	62.5%; Pred. No. 3.ee+02;
	Matches	5; Conservative 0; Mismatches 3; Indels 0; Gaps 0.
OY	2 FGYNRSKF 9	
Dd	5 FGYSKRF 12	
RESULT 14		
ID	AAM33942 standard; peptide; 14 AA.	
AA	AAM33942	
XX		
AC	AAM33942;	
DT	28-MAY-1998 (first entry)	
XX		
DE	Beta1-adrenergic receptor antagonist.	
XX		
KM	Antagonist: integral membrane protein; inhibitor; transmembrane domain;	
KM	therapy; psychotic disorder; Huntington's disease; Parkinson's disease;	
KM	post-myocardial infarction; HIV infection; cell proliferation disorder;	
KW	peptic ulcer; glaucoma; asthma; renal disease; autoimmune disease;	
KW	antibacterial; beta1-adrenergic receptor.	
XX		
OS	Homo sapiens.	
PM	WO9735981-A2.	
PD	02-OCT-1997.	
PF	26-MAR-1997; 97WO-CA000203.	
PR	27-MAR-1996; 96US-0014306P.	
PR	25-JUN-1996; 96US-00670119.	
XX	20-AUG-1996; 96US-0024240P.	
PA	(NGSY/) NG G Y K.	
PA	(SEEM/) SEEMAN P.	
PA	(GEOR/) GEORGE S R.	
PA	(ODOW/) O'DOWD B F.	
P1	Ng GYK, Seeman P, George SR, Odowd BF;	
DR	WPt; 1997-489566/45.	
PT	Inhibitor of integral membrane protein - used to treat e.g.	
PT	schizophrenia, hypertension, viral infection, cancer etc.	
PS	Claim 17; Page 94; 127pp; English.	
XX		
CC	This sequence is a beta1-adrenergic receptor antagonist, and is an	
CC	antagonist of the invention. The antagonists (A) are for inhibiting the	
CC	function of a prokaryotic or eukaryotic integral membrane protein (IMP)	
CC	having at least one transmembrane domain (TMD), comprises a peptide of	
CC	including at least 4 consecutive amino acids (aa) from the sequence of	
CC	the TMD. (A) are used to treat or prevent disorders in mammals that	
CC	involve disturbances of IMP, and the same effect is achieved by inserting	
CC	a nucleic acid encoding (A) into the cells of the mammal. Specified	
CC	conditions that can be treated are schizophrenia, psychotic disorders,	
CC	Huntington's disease, Tourette's syndrome, hypertension, post-myocardial	
CC	infarction, tachyarrhythmia, human immunodeficiency virus infection,	
CC	AIDS, cell proliferation (cancer, psoriasis or hyperkeratosis) and drug	
CC	abuse. (A) can also be used to treat peptic ulcer, glaucoma, asthma,	
CC	renal disease, Parkinson's disease, congestive heart failure, migraine,	
CC	depression, obesity, diabetic neuropathy/retinopathy, autoimmune	
CC	diseases, graft rejection etc. (A) can be used as diuretics and	
CC	antibacterials. (A) may also be used to determine function of orphan	
CC	receptors and, when attached to a marker, for tissue imaging to	
CC	localise/quantify specific receptors. The transgenic animals are used to	


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XX XX WO200238796-A2.
XX XX
XX PD 16-MAY-2002.
XX XX
XX PF 08-NOV-2001; 2001WO-US046777.
XX XX
XX PR 08-NOV-2000; 2000US-0246815P.
XX XX
XX PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX XX
XX PI Turk BE, Cantley LC;
XX XX
XX DR WPI; 2002-519316/55.
XX XX
XX PT Rapid determination of protease cleavage site motifs using a mixture-
XX PT based oriented peptide library.
XX XX
XX PS Example 8; Page 52; 126pp; English.
XX XX
XX CC The invention relates to a method for determining an amino acid sequence
XX CC motif for a cleavage site of a protease. The method comprises contacting
XX CC the protease with a peptide library containing degenerate residues which
XX CC allow for cleavage of a substrate by the protease, allowing the protease
XX CC to cleave peptides within the degenerate peptide library having a
XX CC cleavage site for the protease to form a population of cleaved peptides,
XX CC and determining an amino acid sequence motif for the cleavage site of the
XX CC protease. The protease of the method is a matrix metalloproteinase, or a
XX CC proteolytic enzyme that mediates the pathogenesis of a pathogen. The
XX CC protease is a lethal factor of B. anthracis, p1a and YopJ proteases of
XX CC Yersinia, and the smallpox HIL metalloprotease. The protease of the
XX CC invention is selected from a protease of pathogenic organisms, cathepsin
XX CC family protease, tumour necrosis factor-alpha converting enzyme (TACE),
XX CC calpains, caspases, beta-site amyloid precursor protein cleaving enzyme
XX CC (BACE, beta-secretase), presenilins, membrane-type serine proteases,
XX CC furin and other proprotein convertases, proteasome components and
XX CC proteases affecting the blood clotting cascade. The protease inhibitors
XX CC of the invention are useful to treat diseases, including pathogenic
XX CC infections, cancer, and inflammatory diseases. This sequence represents a
XX CC peptide sequence relating to the protease cleavage site motifs of the
XX CC invention
XX XX
XX SQ Sequence 12 AA;
XX XX
XX Query Match 51.0%; Score 26; DB 5; Length 12;
XX XX Best Local Similarity 57.1%; Pred. No. 5.5e+02;
XX XX Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX XX
XX QY 2 FGYNKSK 8
XX XX |||||
XX XX 5 FGYNKSK 11
XX XX
XX DB
XX XX
XX RESULT 18
XX XX AAM97164
XX XX ID AAM97164 standard; peptide; 14 AA.
XX XX
XX AC AAM97164;
XX XX
XX DT 24-JAN-2002 (first entry)
XX XX
XX DE Human peptide #439 encoded by a SNP oligonucleotide.
XX XX
XX KW Immunosuppressive; immunostimulatory; antiinflammatory; cytosolic;
XX KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
XX KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
XX KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
XX KW complement related protein; cytochrome; kinesin; cytokine; interferon;
XX KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
XX KW multifactorial disease; autoimmune disease; infection;
XX KW nervous system disease.
XX XX
XX OS Homo sapiens.
```

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XX XX WO200147944-A2.
XX XX
XX PD 05-JUL-2001.
XX XX
XX PF 28-DEC-2000; 2000WO-US035498.
XX XX
XX PR 28-DEC-1999; 99US-0173419P.
XX XX
XX PR 27-DEC-2000; 2000US-00173419.
XX XX
XX PA (CURA-) CURAGEN CORP.
XX XX
XX PI Shimkels RA, Leach M;
XX XX
XX DR WPI; 2001-465210/50.
XX XX
XX PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
XX PT autoimmune diseases and infections.
XX XX
XX PS Disclosure; Page 3764; 4143pp; English.
XX XX
XX CC The present invention relates to oligonucleotides (see A1U26793-A1U34659)
XX CC encoding polymorphic variants of proteins related to amylases, amyloid
XX CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
XX CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
XX CC complement related proteins, cytochromes, kinesins, cytokines,
XX CC interleukins, interferons, G-protein coupled receptors and thioesterases.
XX CC The present sequence is a peptide encoded by one such oligonucleotide.
XX CC The oligonucleotides and the peptides encoded by them may be used in the
XX CC prevention, diagnosis and treatment of diseases associated with
XX CC inappropriate expression of the proteins listed above. Disorders that may
XX CC be prevented, diagnosed and/or treated include multifactorial diseases
XX CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
XX CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
XX CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
XX CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
XX CC system and an infection of pathogenic organisms
XX XX
XX SQ Sequence 14 AA;
XX XX
XX Query Match 51.0%; Score 26; DB 4; Length 14;
XX XX Best Local Similarity 55.6%; Pred. No. 6.5e+02;
XX XX Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX XX
XX QY 1 GFGYNKSKF 9
XX XX |||||
XX XX 3 GAGEYDNKKF 11
XX XX
XX DB
XX XX
XX RESULT 19
XX XX AAM99539
XX XX ID AAM99539 standard; peptide; 14 AA.
XX XX
XX AC AAM99539;
XX XX
XX DT 07-DEC-2001 (first entry)
XX XX
XX DE Vaccine related MHC ligand peptide SEQ ID NO:642.
XX XX
XX KW Glutamic acid; glutamine; vaccine; major histocompatibility complex; MHC;
XX KW immunomodulator; antiallergic; endocrine; neuroprotectant; virucidal;
XX KW bactericidal; antiparasitic; fungicidal; cytostatic; medicine;
XX KW pharmaceutical; immune disorder; immune deficiency; autoimmune;
XX KW hypersensitivity; allergy; graft rejection; infection; hormonal disorder;
XX KW central nervous system disease; cancer; melanoma; anti-melanoma vaccine;
XX KW human immunodeficiency virus.
XX XX
XX OS Clostridium tectani.
XX XX
XX PN WO200170772-A2.
XX XX
XX PD 27-SEP-2001.
```

XX 22-MAR-2001; 2001WO-FR000872.
 XX PF
 XX 23-MAR-2000; 2000FR-00003711.
 XX PR
 XX (FABR) FABRE MEDICAMENT SA PIERRE.
 XX PA
 XX Klingner-Hamou C, Corvaia N, Beck A, Goetsch L,
 XX PI
 XX WPI; 2001-611470/70.
 XX DR
 XX Stabilized pharmaceutical containing N-terminal glutamic acid or
 XX PT glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt
 XX PT with strong acid.
 XX PS
 XX Claim 9; Page 140; 149pp; French.
 XX CC
 XX The present invention describes a pharmaceutical compound (I) that
 XX CC contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue in
 XX CC the form of an addition salt with a strong, physiologically acceptable
 XX CC acid (II). Also described are: (a) a pharmaceutical composition
 XX CC containing at least one (I); (b) a vaccine containing at least one (I)
 XX CC where this is a major histocompatibility complex (MHC) ligand (Ia); (c) a
 XX CC method for in vitro diagnosis of diseases associated with the presence of
 XX CC (Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process
 XX CC for preparing (I). (I) has immunomodulator, endocrine, antiallergic,
 XX CC neuroprotectant, virucidal, bactericidal, antiparasitic, fungicidal, and
 XX CC cytostatic activities. (I) are useful, in human or veterinary medicine,
 XX CC in pharmaceutical compositions (for treating immune disorders, e.g.
 XX CC immune deficiency, autoimmune states, hypersensitivity, allergy, graft
 XX CC rejection, infection, hormonal disorders and central nervous system
 XX CC diseases), also, where (I) is a MHC ligand (Ia), in vaccines for
 XX CC treatment or prevention of: (i) viral, bacterial, parasitic or fungal
 XX CC infections; or (ii) of cancers. A particular application is in anti-
 XX CC melanoma vaccines. (I) are also useful for in vitro diagnosis of diseases
 XX CC associated with interactions between MHC and (I), e.g. melanoma and human
 XX CC immunodeficiency virus infection. AAM98898 and AAM9592 represent peptides
 XX CC which can be used in pharmaceutical compounds from the present invention
 XX SQ
 XX Sequence 14 AA;
 XX
 XX Query Match 51.0%; Score 26; DB 4; Length 14;
 XX Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX Db 5 KNSKF 9
 XX | | | | |
 XX 5 KNSKF 9
 XX
 XX RESULT 20
 XX ADB71196
 XX ID ADB71196 standard; peptide; 14 AA.
 XX AC
 XX ADB71196;
 XX
 XX 04-DEC-2003 (first entry)
 XX DT
 XX Human modified protein C peptide SEQ ID NO:42.
 XX DE
 XX variant blood coagulation component; anticoagulant; protein C;
 XX KM activated protein C; blood; thrombolytic; anticoagulant;
 XX KM coagulation disorder; thrombosis; mutant; variant.
 XX XX
 XX Synthetic.
 XX OS Homo sapiens.
 XX XX
 XX MO2003073980-A2.
 XX PN
 XX 12-SEP-2003.
 XX PD
 XX 28-FEB-2003; 2003WO-SE000331.
 XX PF
 XX XX

PR 01-MAR-2002; 2002US-0360181P.
 PR 06-AUG-2002; 2002US-0401042P.
 PR (TACT-) TAC THROMBOSIS & COAGULATION AB.
 XX PA
 XX Dahnbaeck B;
 XX PI
 XX WPI; 2003-722004/68.
 XX DR
 XX New variant blood coagulation component substantially homologous to
 XX PT protein C or activated protein C useful for preparing a composition for
 XX PT treating or preventing coagulation disorders.
 XX PS
 XX Example 1; Page 46; 113pp; English.
 XX CC
 XX The present invention describes a variant blood coagulation component (I)
 XX CC which is substantially homologous in amino acid sequence to a wild-type
 XX CC anticoagulant protein in the protein C-anticoagulant system selected from
 XX CC protein C (PC) and activated protein C (APC). (I) exhibits enhanced
 XX CC anticoagulant activity compared to the wild-type blood component, and
 XX CC comprises at least one amino acid sequence modification in its 45 N-
 XX CC terminal amino acids (the Gla-domain), and at least one amino acid
 XX CC sequence modification in a region corresponding to the serine-protease
 XX CC (SP) domain of the wild-type protein. Also described: (1) a DNA segment
 XX CC comprising a nucleotide sequence encoding (1); (2) a DNA vector
 XX CC (especially an expression vector) comprising the DNA segment of (1); (3)
 XX CC a microorganism or (preferably an) animal host cell stably transfected
 XX CC with the vector of (2); (4) producing the DNA segment coding for the
 XX CC variant blood coagulation component by introducing mutations into the
 XX CC wild-type DNA and replicating the modified DNA produced; (5) producing
 XX CC (1) from a culture of the transfected host cell; (6) a diagnostic test
 XX CC system, especially a kit, for assaying components participating in the
 XX CC protein C-anticoagulant system of blood, comprising (1); and (7)
 XX CC inhibiting coagulation in a patient by administering a composition
 XX CC containing (I). (I) has thrombolytic and anticoagulant activities. The
 XX CC variant blood coagulation component (I) is useful in the manufacture of a
 XX CC medicament for treating or preventing coagulation disorders, such as
 XX CC thrombosis. The medicament is especially suitable for treating a patient
 XX CC with APC resistance. The assay system is useful for assaying components
 XX CC participating in the protein C-anticoagulant system of blood. The
 XX CC variants exhibit increased anticoagulant activity compared to the wild-
 XX CC type protein. The present sequence represents a human modified protein C
 XX CC peptide, which is given in the exemplification of the present invention.
 XX SQ
 XX Sequence 14 AA;
 XX
 XX Query Match 51.0%; Score 26; DB 7; Length 14;
 XX Best Local Similarity 50.0%; Pred. No. 6.5e+02;
 XX Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX Db 1 GFGYKSK 8
 XX | | | | |
 XX 3 GWDGHSR 10
 XX
 XX RESULT 21
 XX AAM99439
 XX ID AAM99439 standard; peptide; 9 AA.
 XX AC
 XX AAM99439;
 XX
 XX 07-DEC-2001 (first entry)
 XX DT
 XX Vaccine related MHC ligand peptide SEQ ID NO:542.
 XX DE
 XX Glutamic acid; glutamine; vaccine; major histocompatibility complex; MHC;
 XX KM immunomodulator; antiallergic; endocrine; neuroprotectant; virucidal;
 XX KM bactericidal; antiparasitic; fungicidal; cytostatic; medicine;
 XX KM pharmaceutical; immune disorder; immune deficiency; autoimmune;
 XX KM hypersensitivity; allergy; graft rejection; infection; hormonal disorder;
 XX KM central nervous system disease; cancer; melanoma; anti-melanoma vaccine;
 XX KM human immunodeficiency virus.
 XX XX

OS Homo sapiens.
 XX
 PN WO200170772-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 22-MAR-2001; 2001WO-FR000872.
 XX
 PR 23-MAR-2000; 2000FR-00003711.
 XX
 PA (FABR) FABRE MEDICAMENT SA PIERRE.
 XX
 PI Klinguer-Hamour C, Corvaia N, Beck A, Goetsch L;
 XX
 DR WPI; 2001-611470/70.
 XX
 PT Stabilized pharmaceutical containing N-terminal glutamic acid or
 PT glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt
 PT with strong acid.
 XX
 PS Claim 9; Page 123; 149pp; French.
 XX
 CC The present invention describes a pharmaceutical compound (I) that
 CC contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue in
 CC the form of an addition salt with a strong, physiologically acceptable
 CC acid (II). Also described are: (a) a pharmaceutical composition
 CC containing at least one (I); (b) a vaccine containing at least one (I)
 CC where this is a major histocompatibility complex (MHC) ligand (Ia); (c) a
 CC method for in vitro diagnosis of diseases associated with the presence of
 CC (Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process
 CC for preparing (I). (I) has immunomodulator, endocrine, antiallergic,
 CC neuroprotectant, virucidal, bactericidal, antiparasitic, fungicidal and
 CC cytostatic activities. (I) are useful, in human or veterinary medicine,
 CC in pharmaceutical compositions (for treating immune disorders, e.g.
 CC immune deficiency, autoimmune states, hypersensitivity, allergy, graft
 CC rejection, infection, hormonal disorders and central nervous system
 CC diseases), also, where (I) is a MHC ligand (Ia), in vaccines for
 CC treatment or prevention of: (i) viral, bacterial, parasitic or fungal
 CC infections; or (ii) of cancers. A particular application is in anti-
 CC melanoma vaccines. (I) are also useful for in vitro diagnosis of diseases
 CC associated with interactions between MHC and (I), e.g. melanoma and human
 CC immunodeficiency virus infection. AAM98898 to AAM99592 represent peptides
 CC which can be used in pharmaceutical compounds from the present invention
 CC
 SQ Sequence 9 AA:
 XX
 XX
 Query Match 49.0%; Score 25; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GFGY 4
 ||||
 Db 4 GFGY 7
 RESULT 22
 AAM99577
 ID AAM99577 standard; peptide; 9 AA.
 XX
 AC AAM99577;
 XX
 DT 07-DEC-2001 (first entry)
 XX
 DE Vaccine related MHC ligand peptide SEQ ID NO:680.
 XX
 KW Glutamic acid; glutamine; vaccine; major histocompatibility complex; MHC;
 KW immunomodulator; antiallergic; endocrine; neuroprotectant; virucidal;
 KW bactericidal; antiparasitic; fungicidal; cytostatic; medicine;
 KW pharmaceutical; immune disorder; immune deficiency; autoimmune;
 KW hypersensitivity; allergy; graft rejection; infection; hormonal disorder;
 KW central nervous system disease; cancer; melanoma; anti-melanoma vaccine;
 KW human immunodeficiency virus.
 XX

OS Homo sapiens.
 XX
 PN WO200170772-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 22-MAR-2001; 2001WO-FR000872.
 XX
 PR 23-MAR-2000; 2000FR-00003711.
 XX
 PA (FABR) FABRE MEDICAMENT SA PIERRE.
 XX
 PI Klinguer-Hamour C, Corvaia N, Beck A, Goetsch L;
 XX
 DR WPI; 2001-611470/70.
 XX
 PT Stabilized pharmaceutical containing N-terminal glutamic acid or
 PT glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt
 PT with strong acid.
 XX
 PS Claim 9; Page 146; 149pp; French.
 XX
 CC The present invention describes a pharmaceutical compound (I) that
 CC contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue in
 CC the form of an addition salt with a strong, physiologically acceptable
 CC acid (II). Also described are: (a) a pharmaceutical composition
 CC containing at least one (I); (b) a vaccine containing at least one (I)
 CC where this is a major histocompatibility complex (MHC) ligand (Ia); (c) a
 CC method for in vitro diagnosis of diseases associated with the presence of
 CC (Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process
 CC for preparing (I). (I) has immunomodulator, endocrine, antiallergic,
 CC neuroprotectant, virucidal, bactericidal, antiparasitic, fungicidal and
 CC cytostatic activities. (I) are useful, in human or veterinary medicine,
 CC in pharmaceutical compositions (for treating immune disorders, e.g.
 CC immune deficiency, autoimmune states, hypersensitivity, allergy, graft
 CC rejection, infection, hormonal disorders and central nervous system
 CC diseases), also, where (I) is a MHC ligand (Ia), in vaccines for
 CC treatment or prevention of: (i) viral, bacterial, parasitic or fungal
 CC infections; or (ii) of cancers. A particular application is in anti-
 CC melanoma vaccines. (I) are also useful for in vitro diagnosis of diseases
 CC associated with interactions between MHC and (I), e.g. melanoma and human
 CC immunodeficiency virus infection. AAM98898 to AAM99592 represent peptides
 CC which can be used in pharmaceutical compounds from the present invention
 CC
 SQ Sequence 9 AA:
 XX
 XX
 Query Match 49.0%; Score 25; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GFGY 4
 ||||
 Db 6 GFGY 9
 RESULT 23
 AAM28520
 ID AAM28520 standard; peptide; 10 AA.
 XX
 AC AAM28520;
 XX
 DT 11-JAN-1998 (first entry)
 XX
 DE Human Herpes VI sequence.
 XX
 KW Biosensor; capture; ligand; ion; electron; channel; current;
 KW Herpes virus.
 KW
 OS Synthetic.
 XX
 PN AT9501943-A.
 XX
 PD 15-APR-1997.
 XX

XX 28-NOV-1995; 95AT-00001943.
 PF 28-NOV-1995; 95AT-00001943.
 PR 28-NOV-1995; 95AT-00001943.
 XX
 PA (SCHA/) SCHALKHAMMER T.
 PA (PIRT/) PIRTNER F.
 XX
 DR WPI; 1997-272445/25.
 XX
 PT Bio-sensor for nucleic acid determination - with capture ligands
 PT immobilised in ion channels in membrane.
 XX
 PS Example 12; Page 9; 17pp; German.
 XX
 CC Example 12 describes the prodn. of a Herpes virus biosensor where the
 CC capture ligands (Oligonucleotides) are based on the sequences given in
 CC AAW8515-W8526. The biosensor is useful for determining DNA or RNA
 CC concentrations by a method comprising measuring changes in ion and/or
 CC electron current induced by hybridisation in the channels
 XX
 SQ Sequence 10 AA;
 Query Match 49.0%; Score 25; DB 2; Length 10;
 Best Local Similarity 57.1%; Pred. No. 7e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GFGYKNS 7
 Db 3 GIGYKGA 9
 RESULT 24
 AAW63824
 ID AAW63824 standard; peptide; 10 AA.
 AC AAW63824;
 DT 28-SEP-1998 (first entry)
 XX
 DE Human Mab #117-10C heavy chain CDR3 peptide fragment.
 XX
 KW Interleukin-18; IL-18; human; treatment; autoimmune disease; Mab;
 KW immunosuppressant; inhibitor; receptor protein; detection; heavy chain;
 KW monoclonal antibody; Mab; complementarily determining region; CDR3.
 XX
 OS Homo sapiens.
 XX
 PN EP850952-A1.
 PD 01-JUL-1998.
 XX
 PF 23-DEC-1997; 97EP-00310555.
 XX
 PR 26-DEC-1996; 96JP-00356426.
 PR 21-FEB-1997; 97JP-00052526.
 PR 06-JUN-1997; 97JP-00163490.
 PR 28-JUL-1997; 97JP-00215490.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 PI Torigoe K, Ushio S, Kunikata T, Kurimoto M;
 XX
 DR WPI; 1998-335317/30.
 XX
 PT New interleukin-18 receptor protein - used to inhibit interleukin-18, to
 PT treat autoimmune disease and as immunosuppressant to treat e.g. graft
 PT rejection, insulin-resistant diabetes and ulcerative colitis.
 XX
 PS Claim 14; Page 20; 35pp; English.
 XX
 CC This sequence represents the human monoclonal antibody (Mab) #117-10C
 CC heavy chain complementarity determining region, CDR3 which is used in a

CC method involved in neutralising IL-18 or to treat autoimmune diseases or
 CC as an immunosuppressant using anti-IL-18 antibodies which can inhibit IL-
 CC 18. Such antibodies can also be used to detect the IL-18 receptor protein
 CC (labeled with an enzyme or a radioactive or fluorescent substance). The
 CC protein is used to treat e.g. graft rejection, pernicious anaemia,
 CC atrophic gastritis, insulin-resistant diabetes, Wegener's granulomatosis,
 CC discoid lupus erythematosus, ulcerative colitis, cold-agglutinin-relating
 CC diseases, Goodpasture's syndrome, primary biliary cirrhosis, sympathetic
 CC ophthalmitis, hyperthyroidism, juvenile onset type diabetes, Sjogren
 CC syndrome, autoimmune hepatitis, autoimmune haemolytic anaemia, myasthenia
 CC gravis, systemic scleroderma, systemic lupus erythematosus, polypletic
 CC cold haemaglobinuria, polymyositis, periarthritis nodosa, multiple
 CC sclerosis, Addison's disease, purpura haemorrhagica, Basedow's disease,
 CC leukopaemia, Behcet's disease, climacterium praecox, rheumatoid
 CC arthritis, rheumatopyra, chronic thyroiditis, Hodgkin's disease, HIV,
 CC asthma, atopic dermatitis, allergic nasitis, pollinosis, apltoksin-
 CC allergy and septic shock resulting from production or administration of
 CC excessive gamma interferon (IFN-gamma)
 XX
 SQ Sequence 10 AA;
 Query Match 49.0%; Score 25; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GFGY 4
 Db 7 GFGY 10
 RESULT 25
 AAB46262
 ID AAB46262 standard; peptide; 10 AA.
 AC AAB46262;
 DT 04-APR-2001 (first entry)
 XX
 DE HPV type 16 cytotoxic T-cell epitope SEQ ID NO 17.
 XX
 KW Cytotoxic T cell; epitope; LI protein; antiviral; antitumor; antigen;
 KW vaccine; tumor; protective immune response.
 XX
 OS Human papillomavirus.
 XX
 PN DE19925235-A1.
 PD 07-DEC-2000.
 XX
 PF 01-JUN-1999; 99DE-01025235.
 XX
 PR 01-JUN-1999; 99DE-01025235.
 XX
 PA (MEDT-) MEDIGENE AG.
 PA (DKFZ-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM.
 XX
 PI Schaefer K, Faath S, Jochmus I, Nieland J, Osen W;
 XX
 DR WPI; 2001-062580/08.
 XX
 PT New T cell epitopes from the papilloma virus LI protein, useful for
 PT detecting or inducing an immune response, e.g. in vaccines.
 XX
 PS Example 4; Page 18; 26pp; German.
 XX
 CC This invention describes novel T cell epitopes (A) of the human papilloma
 CC virus LI protein. The invention also describes (a) compounds (II)
 CC containing an (A) provided it is not a natural LI protein nor an
 CC exclusively N- or C-terminal deletion variant of natural LI; (b) nucleic
 CC acid (III) that encodes (A) or (I); (c) vector, particularly an expression
 CC vector, that contains (II); (d) cells that contain, and preferably
 CC present, (A); (e) complex of (A) or (I) with at least one additional
 CC molecule (III); in vitro detection of T cell activation by a compound

XX 18-JUN-2001 (first entry)
XX Synthetic peptide, SEQ ID NO: 9.
DE Peptidomimetic; beta-hairpin loop mimetic; binding motif identification;
XX drug design; protein target identification.
KM Synthetic.
OS WO200116161-A1.
XX 08-MAR-2001.
PD 30-AUG-1999; 99WO-EP006369.
PF 30-AUG-1999; 99WO-EP006369.
PR (POLY-) POLYPHOR AG.
XX Robinson DA, Obrecht D;
PI WPI; 2001-273332/28.
XX Method for manufacturing template-fixed beta-hairpin loop mimetics,
PT useful for designing small peptidomimetic drug candidates, involves
PT process based on mixed solid and solution phase synthetic strategy.
XX Claim 7; Page 77; 83pp; English.
PS The present sequence is part of a template-fixed, beta-hairpin loop
CC peptidomimetic which may be manufactured by the process disclosed in this
CC invention. The process is based on a mixed solid and solution phase
CC synthetic strategy. The method is useful for determining key amino acids
CC and motifs important for binding large surface and flat protein
CC interfaces in their sequential and/or spatial arrangement. This
CC information can ultimately be used for the design of small peptidomimetic
CC drug candidates. The peptidomimetics may be used to probe large surface
CC protein-protein interactions and to find protein targets
CC
SQ Sequence 12 AA;
Query Match 49.0%; Score 25; DB 4; Length 12;
Best Local Similarity 50.0%; Pred. No. 8.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 2 FGYNKSKF 9
DB 4 YGVKNSEW 11
RESULT 29
ABR74314
ID ABR74314 standard; peptide; 12 AA.
XX ABR74314;
AC 18-APR-2002 (first entry)
DT Simple nuclear localisation signal peptide SEQ ID NO:78.
XX
DE Fungogenic; nuclear localisation signal; NLS; encapsulation; lipogene;
KM liposome; micelle; karyophilic; cytosolic; antitumour; solid tumour;
KM peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;
KM breast carcinoma; prostate carcinoma.
XX Synthetic.
OS WO200193836-A2.
XX PN 13-DEC-2001.
PD 08-JUN-2001; 2001WO-US018657.
PF

XX 09-JUN-2000; 2000US-0210925P.
PR (BOUT/) BOUTIKAS T.
XX
XX Boulikas T;
XX WPI; 2002-164295/21.
DR Encapsulation of plasmid DNA (lipogenes) and therapeutic agents with
PT nuclear localization signal/fungogenic peptide conjugates into targeted
PT liposome complexes.
XX Claim 14; Page 57; 107pp; English.
PS The present invention describes a method for producing micelles with
CC entrapped therapeutic agents. The method comprises: (1) combining
CC negatively charged agent with a cationic lipid in a ratio where 30-90 %
CC of the negatively charged atoms are neutralised by positive charges on
CC lipid molecules to form an electrostatic micelle complex in 20-80 %
CC ethanol; and (2) combining the micelle complex of (a) with fungogenic-
CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing
CC micelles with entrapped therapeutic agents. Also described is a method
CC for delivering a therapeutic agent in vivo, comprising the administration
CC of the micelle. ABR74256 to ABR74858 represent specifically claimed
CC nuclear localisation signal (NLS) peptides for use in the method as the
CC fungogenic-karyophilic peptides. The micelles produced can have cytostatic
CC and antitumour activities. The peptide-lipid-polynucleotide complexes
CC produced are useful for inhibiting the progression of neoplastic
CC diseases. The invention relates to the field of gene therapy and is
CC directed toward methods for producing peptide-lipid-polynucleotide
CC complexes suitable for delivery of polynucleotides. The encapsulated
CC molecules display therapeutic efficacy in eradicating solid tumours
CC including but not limited to breast carcinoma or prostate carcinoma.
CC ABR74235 to ABR74255 are used in the exemplification of the present
CC invention
XX
SQ Sequence 12 AA;
Query Match 49.0%; Score 25; DB 5; Length 12;
Best Local Similarity 50.0%; Pred. No. 8.4e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 GFGYNKSK 8
DB 2 GYGDNRNK 9
RESULT 30
AAE28582
ID AAE28582 standard; peptide; 12 AA.
XX AAE28582;
AC 27-DEC-2002 (first entry)
DT Desmodium uncinatum leucoanthocyanidin reductase (LAR) peptide #5.
XX
DE Leucoanthocyanidin reductase; LAR; reductase-epimerase-dehydrogenase;
KM RBP; proanthocyanidin; pasture quality; legume; bloat-safe forage crop;
KM disease resistance; pest resistance; enzyme.
XX Desmodium uncinatum.
OS Key Location/Qualifiers
XX FH Misc-difference 1 /label= Leu, Ile
FT Misc-difference 9 /label= Leu, Ile
FT Misc-difference 10 /label= Leu, Ile
FT
XX WO200266625-A1.
PN


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XX 29-AUG-2002.
PD
XX
XX 21-FEB-2002; 2002WO-AU000179.
PF
XX
XX 21-FEB-2001; 2001AU-00003241.
PR
XX
XX (CSTR ) COMMONWEALTH SCI & IND RES ORG.
PA (MEAT-) MEAT & LIVESTOCK AUSTRALIA LTD.
XX
XX Tanner GJ, Ashton AR, Abrahams S, Watson JM, Larkin PJ,
PI Franckl KT;
XX
XX WPI; 2002-691619/74.
DR
XX
XX New LAR polypeptide from the R2D protein superfamily, useful for
PT regulating the biosynthesis and accumulation of proanthocyanidins in
PT plants, and modifying the pasture quality of legumes.
XX
XX Claim 6; Page 135; 175pp; English.
XX
XX The present invention relates to novel leucoanthocyanidin reductase (LAR)
CC proteins of reductase-epimerase-dehydrogenase (RED) protein superfamily
CC and polynucleotides encoding such proteins. LAR sequences are useful for
CC regulating the biosynthesis and accumulation of proanthocyanidins in
CC plants. They are useful for modifying the pasture quality of legumes, in
CC particular to produce bioat-safe forage crops or crops having enhanced
CC nutritional value, enhanced disease resistance or pest resistance or
CC enhanced matting qualities. The present sequence is Desmodium uncinatum
CC LAR peptide
XX
XX SQ
XX
XX Sequence 12 AA;
XX
XX Query Match 49.0%; Score 25; DB 5; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 8.4e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GFGY 4
XX ||||
XX Db 2 GFGY 5
XX
XX
XX RESULT 31
XX AAW94978
XX ID AAW94978 standard; peptide; 13 AA.
XX
XX AAW94978;
XX AC
XX 12-MAY-1999 (first entry)
XX DT
XX
XX MHC binding peptide from myelin basic protein (MBP).
DE
XX Major histocompatibility class II; MHC; binding; vaccine; MBP;
XX autoimmune disease; myelin basic protein; HLA-DRB1*0401.
XX
XX OS
XX Synthetic.
XX
XX WO9659244-A1.
XX PN
XX 30-DEC-1998.
XX PD
XX 19-JUN-1998; 98WO-GB001801.
XX PF
XX 20-JUN-1997; 97GB-00012892.
XX PR
XX (ECLA-) ECLAGEN LTD.
XX PA
XX Fothergill J, Kemp G, Brooks T, Carr F;
XX WPI; 1999-105639/09.
XX
XX Identifying MHC binding peptides - by ascertaining the characteristics of
XX a MHC molecule binding groove and determining conformation scores of
XX

```

```

PT pocket bound peptides.
XX
XX Example 4; Page 50; 64pp; English.
XX
XX The invention relates to a method for the prediction of the binding
CC affinity of a peptide to major histocompatibility (MHC) class II
CC molecules. The method comprises (a) ascertaining the characteristics of a
CC MHC molecule binding groove; (b) presenting a selected peptide to the MHC
CC molecule and ascertaining a first conformation score for each pocket
CC bound peptide side-chain; (c) amending the conformation of each pocket
CC bound peptide side-chain and ascertaining a second conformation score;
CC (d) repeating (c) with alternative conformations of each peptide pocket
CC bound side-chain; (e) choosing the highest conformation score for each
CC pocket bound peptide side-chain in each binding groove pockets, and (f)
CC combining the highest conformation score for each pocket and ascertaining
CC a binding score for the complete peptide. The invention also provides a
CC computer conditioned to receive information characterising a peptide
CC bound to the MHC molecule and to utilise the information to predict the
CC binding affinity of the peptide. The method can be used to identify
CC peptides in a protein which can bind to a given MHC molecule. Such
CC peptides can be used in the production of molecules for use in e.g.
CC vaccines, autoimmune diseases and diagnostics. Sequences AAW94957 to
CC AAW94981 represent peptides from myelin basic protein (MBP) that can bind
XX with MHC molecule HLA-DRB1*0401
XX
XX SQ
XX
XX Sequence 13 AA;
XX
XX Query Match 49.0%; Score 25; DB 2; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 9.1e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GFGY 4
XX ||||
XX Db 2 GFGY 5
XX
XX
XX RESULT 32
XX AAB13279
XX ID AAB13279 standard; peptide; 13 AA.
XX
XX AAB13279;
XX AC
XX 12-JAN-2001 (first entry)
XX DT
XX
XX Caenorhabditis elegans conserved sequence #27.
DE
XX
XX Caenorhabditis elegans; metabolic enzyme; AKT kinase; daf-18;
XX insulin signalling pathway; daf-2; age-1; insulin receptor; PI 3-kinase;
XX PKB kinase; PTEN lipid phosphatase; antidiabetic; obesity;
XX diabetes.
XX
XX Caenorhabditis elegans.
XX OS
XX WO200033068-A1.
XX PN
XX 08-JUN-2000.
XX PD
XX 02-DEC-1999; 99WO-US028529.
XX PF
XX 03-DEC-1998; 98US-00205658.
XX PR
XX (GEHO ) GEN HOSPITAL CORP.
XX PA
XX Ruvkun G, Ogy S;
XX WPI; 2000-423022/36.
XX
XX Diagnosing and treating obesity and impaired glucose tolerance using
XX modulators of daf-18 expression and/or activity.
XX
XX Disclosure; Page 171; 402pp; English.
XX
XX The present sequence is conserved protein region of a Caenorhabditis
XX

```

CC elegans homologue of a key metabolic enzyme. A number of *C. elegans* genes
 CC have been identified as homologues of genes in the mammalian insulin
 CC signalling pathway. The *C. elegans* age-1 gene encodes a homologue of the
 CC mammalian PI 3-kinase whilst *dat-2* encodes a homologue of the mammalian
 CC insulin receptor. The *C. elegans* AKT kinase and PKB kinase act downstream
 CC of *dat-2* and age-1, just as their mammalian homologues act downstream of
 CC insulin signalling. The *C. elegans* PTEN lipid phosphatase homologue, DAF-
 CC 18, has been found to act upstream of AKT in the pathway. This discovery
 CC has enabled mammalian PTEN action to be mapped to the insulin signalling
 CC pathway. Conserved DAF motifs can be used to design probes to identify
 CC mammalian DAF homologues and thus to identify individuals with a
 CC predisposition toward the development of glucose intolerance conditions,
 CC such as obesity and diabetes

SO Sequence 13 AA;

Query Match 49.0%; Score 25; DB 3; Length 13;
 Best Local Similarity 66.7%; Pred. No. 9.1e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GFGYKN 6
 |||||
 DB 2 GFGWKN 7

RESULT 33
 ADD44065
 ID ADD44065 standard; peptide; 13 AA.
 XX
 AC ADD44065;

15-JAN-2004 (first entry)

CPG2 peptide #85 with potential human MHC class II binding activity.

bacterial enzyme; carboxypeptidase G2; CPG2; non-immunogenic;
 immunogenic; T-cell epitope; MHC class II binding ligand;

immunostimulant; enzyme therapy; immune response;
 gene directed enzyme prodng strategy; vaccine; enzyme; EC 3.4.17.11.

Pseudomonas sp. RS-16.

WO2003045426-A1.

05-JUN-2003.

27-NOV-2002; 2002WO-EP013351.

29-NOV-2001; 2001EP-00128519.

25-JAN-2002; 2002EP-00001778.

13-SEP-2002; 2002EP-00020634.

(MERE) MERCK PATENT GMBH.

Hellendoorn K, Baker M, Williams S, Carr FU;

WPI; 2003-513617/48.

New modified bacterial enzyme carboxypeptidase G2 (CPG2) having
 substantially non-immunogenic or less immunogenic than any non-modified
 CPG2, useful for inducing an immune response in a human host.

Claim 3; Page 13; 52pp; English.

The invention relates to a novel modified bacterial enzyme
 carboxypeptidase G2 (CPG2). The modified enzyme can result in CPG2
 proteins that are substantially non-immunogenic or less immunogenic than
 any non-modified CPG2 having essentially the same biological specificity
 when used in vivo, and comprising specific amino acid residues having
 alterations compared with the non-modified parental enzyme. The
 alterations cause a reduction or an elimination of one or more of T-cell
 epitope sequences, which act in the parental enzyme as MHC class II
 binding ligands and stimulate T-cells. The modified CPG2 enzyme and the

CC CPG2 proteins have immunostimulant activity and may be used in enzyme
 CC therapy. The modified CPG2 enzyme may be used to induce an immune
 CC response in a human host, or as a therapeutic entity such as the gene
 CC directed enzyme prodng strategy. The peptide is useful for the
 CC manufacture of a modified CPG2 enzyme having substantially no or less
 CC immunogenicity than any non-modified parental enzyme when used in vivo,
 CC and for vaccination of patients to reduce immunogenicity to CPG2 in vivo.
 CC This sequence represents a CPG2 enzyme peptide with potential human MHC
 CC class II binding activity of the invention.

SO Sequence 13 AA;

Query Match 49.0%; Score 25; DB 7; Length 13;
 Best Local Similarity 100.0%; Pred. No. 9.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GFGY 4
 |||||
 DB 7 GFGY 10

RESULT 34
 ADD44039
 ID ADD44039 standard; peptide; 13 AA.
 XX
 AC ADD44039;

15-JAN-2004 (first entry)

CPG2 peptide #59 with potential human MHC class II binding activity.

bacterial enzyme; carboxypeptidase G2; CPG2; non-immunogenic;
 immunogenic; T-cell epitope; MHC class II binding ligand;

immunostimulant; enzyme therapy; immune response;
 gene directed enzyme prodng strategy; vaccine; enzyme; EC 3.4.17.11.

Pseudomonas sp. RS-16.

WO2003045426-A1.

05-JUN-2003.

27-NOV-2002; 2002WO-EP013351.

29-NOV-2001; 2001EP-00128519.

25-JAN-2002; 2002EP-00001778.

13-SEP-2002; 2002EP-00020634.

(MERE) MERCK PATENT GMBH.

Hellendoorn K, Baker M, Williams S, Carr FU;

WPI; 2003-513617/48.

New modified bacterial enzyme carboxypeptidase G2 (CPG2) having
 substantially non-immunogenic or less immunogenic than any non-modified
 CPG2, useful for inducing an immune response in a human host.

Claim 3; Page 13; 52pp; English.

The invention relates to a novel modified bacterial enzyme
 carboxypeptidase G2 (CPG2). The modified enzyme can result in CPG2
 proteins that are substantially non-immunogenic or less immunogenic than
 any non-modified CPG2 having essentially the same biological specificity
 when used in vivo, and comprising specific amino acid residues having
 alterations compared with the non-modified parental enzyme. The
 alterations cause a reduction or an elimination of one or more of T-cell
 epitope sequences, which act in the parental enzyme as MHC class II
 binding ligands and stimulate T-cells. The modified CPG2 enzyme and the
 CPG2 proteins have immunostimulant activity and may be used in enzyme
 CC therapy. The modified CPG2 enzyme may be used to induce an immune
 CC response in a human host, or as a therapeutic entity such as the gene
 CC directed enzyme prodng strategy. The peptide is useful for the

CC manufacture of a modified CPg2 enzyme having substantially no or less
 CC immunogenicity than any non-modified parental enzyme when used in vivo,
 CC and for vaccination of patients to reduce immunogenicity to CPg2 in vivo.
 CC This sequence represents a CPg2 enzyme peptide with potential human MHC
 CC class II binding activity of the invention.

CC Sequence 13 AA;

Query Match 49.0%; Score 25; DB 7; Length 13;

Best Local Similarity 100.0%; Pred. No. 9.1e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGY 4
 ||||
 Db 10 GFGY 13

RESULT 35

ADC73226 standard; peptide; 14 AA.

AC ADC73226;

DT 01-JAN-2004 (first entry)

DE Retro osteogenic growth polypeptide fragment.

XX osteogenic growth polypeptide; OGP analogue; osteoblastic;

KM fibroblastic cell production; bone formation; osteopetral fracture;

KM wound; intraosseous implant; osteoporosis; OGP(1-14); OGP(10-14).

OS Synthetic.

PN WO9732594-A1.

XX 12-SEP-1997.

XX 10-MAR-1997; 97WO-IL000087.

XX 10-MAR-1996; 96IL-00117426.

XX (YISS) YISSUM RES & DEV CO.

PI Bab I, Gaiz D, Yu-Chen C, Muhrad A, Shteyer A, Choev M;

DR WPI; 1997-470492/43.

XX New osteogenic growth polypeptide analogues - used e.g. for stimulating
 PT the formation of osteoblastic or fibroblastic cells and treating
 PT conditions requiring enhanced bone cell formation.

PS Example; Page 11; 38pp; English.

CC The invention relates to novel pseudopeptidic osteogenic growth
 CC polypeptide (OGP) analogues. The analogues of the invention may be used
 CC for stimulating the formation of osteoblastic or fibroblastic cells,
 CC enhancing bone formation in osteopetral-related pathological conditions,
 CC repairing fractures, healing wounds, grafting of intraosseous implants
 CC and reversing bone loss in osteoporosis and other conditions requiring
 CC enhanced bone cell formation. Furthermore, the analogues may have
 CC activities similar to or superior to that of the parent oligopeptides
 CC OGP(1-14) and OGP(10-14), as well as increased resistance to peptidase
 CC degradation, longer persistence in circulation or increased potency and
 CC bioavailability. The current sequence is that of the retro osteogenic
 CC growth polypeptide fragment of the invention.

XX Sequence 14 AA;

Query Match 49.0%; Score 25; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 9.8e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGY 4

Db 2 GFGY 5
 ||||

RESULT 36

AAU68422 standard; peptide; 14 AA.

XX AAU68422;

DT 16-JAN-2002 (first entry)

DE Human Breast cancer-associated protein isoform, BPI-249 peptide.

XX Human; Breast cancer-associated protein isoform; breast cancer;

KM Immunogen; cytostatic; BPI; tryptic digest peptide.

XX Homo sapiens.

PN WO200171357-A2.

XX 27-SEP-2001.

XX 20-MAR-2001; 2001WO-GB001219.

XX 20-MAR-2000; 2000GB-00006695.

XX 24-MAR-2000; 2000GB-00007265.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PI Herath HMAC, O'hare MJ, Page MJ, Parekh RB, Waterfield MD;

DR WPI; 2001-611532/70.

XX Identifying proteins for clinical screening, diagnosis and prognosis of
 PT breast cancer, comprises detecting Breast Cancer-Associated Protein
 PT isoforms (BPIs) using two-dimensional electrophoresis.

PS Claim 9; Page 52; 197pp; English.

CC The invention relates to diagnosing, determining the stage or severity,
 CC or identifying the risk of a subject developing cancer (especially breast
 CC cancer), or monitoring the effect of therapy on a subject with cancer,
 CC comprising analysing a test sample using two-dimensional electrophoresis
 CC and detecting Breast Cancer-Associated Protein isoforms (BPIs). The
 CC methods disclosed are used for the diagnosis and prognosis of breast
 CC cancer, for determining the severity of breast cancer, and for
 CC identifying a subject at risk of developing breast cancer, and for
 CC the effect of therapy administered to a subject. Antibodies raised
 CC against the binding domain of a BPI, the binding domain of a BPI, a
 CC nucleic acid encoding a BPI, or a nucleic acid that inhibits the function
 CC of a BPI can be incorporated into a pharmaceutical composition for
 CC treating or preventing breast cancer. The methods use sensitive and
 CC specific biomarkers provide early diagnosis of breast cancer, and the
 CC compositions are more potent, specific, and has a more rapid effect with
 CC fewer side effects than other prior art methods. The present sequence is
 CC a tryptic digest peptide from a BPI of the invention

XX Sequence 14 AA;

Query Match 49.0%; Score 25; DB 4; Length 14;

Best Local Similarity 80.0%; Pred. No. 9.8e+02; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGYN 6
 ||||
 Db 9 FGYN 13

RESULT 37

AAU25297 standard; peptide; 14 AA.

XX

AC AAU25297;
 DT 18-DEC-2001 (first entry)
 XX
 DE Schizophrenia-Associated Protein Isoform (SPI) peptide #526.
 DE Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240;
 KW Schizophrenia; gene therapy; cerebrospinal fluid; serum; plasma.
 XX
 OS Homo sapiens.
 PN WO200162785-A2.
 PD 30-AUG-2001.
 XX
 PF 23-FEB-2001; 2001WO-GB000792.
 XX
 PR 24-FEB-2000; 2000GB-00004415.
 PR 28-DEC-2000; 2000US-00750395.
 XX
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 PI Herath HMC, Parekh RB, Rohlf C, Terrett JA, Tyson XL;
 DR WPI; 2001-570624/64.
 XX
 PT New schizophrenia associated protein isoforms and encoding nucleic acid
 PT molecules, useful for treatment, diagnosis and prognosis of schizophrenia
 PT and screening for potential drugs for treatment and new drug targets.
 PS Disclosure; Page 39; 148pp; English.
 XX
 CC The sequence represents a schizophrenia-associated protein isoform (SPI).
 CC These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable
 CC in cerebrospinal fluid, serum or plasma and are useful markers of
 CC schizophrenia. The sequences can be used for treatment and diagnosis of
 CC schizophrenia. screening, prognosis, monitoring the results of therapy,
 CC identifying patients most likely to respond to a particular therapy and
 CC identification of new targets for drug treatment. SPI DNA is useful as a
 CC nucleic acid probe to detect the presence of nucleic acids or SPIs
 XX
 SQ Sequence 14 AA;
 SO
 QY Query Match 49.0%; Score 25; DB 4; Length 14;
 Best Local Similarity 80.0%; Pred. No. 9.8e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DB 2 FGYN 6
 9 FGYSN 13
 XX
 RESULT 38
 AAU15641
 ID AAU15641 standard; peptide; 14 AA.
 XX
 AC AAU15641;
 DT 24-OCT-2001 (first entry)
 XX
 DE Schizophrenia-associated isoform peptide #526.
 DE Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;
 KW Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;
 KW neurological disorder; neuropathy.
 XX
 OS Homo sapiens.
 PN WO200163293-A2.
 PD 30-AUG-2001.
 XX
 PF 23-FEB-2001; 2001WO-GB000783.
 XX

PR 24-FEB-2000; 2000GB-00004415.
 PR 28-DEC-2000; 2000US-00750395.
 XX
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 PI Herath HMC, Parekh RB, Rohlf C;
 DR WPI; 2001-502868/55.
 XX
 PT Diagnosing and monitoring Schizophrenia by detecting the presence of
 PT Schizophrenia Associated Features and Schizophrenia Associated Protein
 PT Isoforms in samples of cerebrospinal fluid.
 PS Claim 6; Page 39; 160pp; English.
 XX
 CC The invention relates to methods and compositions for screening,
 CC diagnosis and prognosis of Schizophrenia. The method involves detecting
 CC the presence of Schizophrenia (SCH) Associated Features (SFI) and SCH
 CC Associated Protein Isoforms (SPI) in samples, e.g. by electrophoresis,
 CC immunassay or hybridisation assay, for diagnosing and monitoring SCH;
 CC studying the effectiveness of treatments and for identifying potential
 CC therapeutic agents. The method is used for (1) screening or correlates
 CC SCH and the relative abundance of at least 1 chosen feature correlates
 CC with the presence or absence of SCH; and (2) monitoring the effect of
 CC therapy administered to a subject with SCH and the relative abundance of
 CC at least 1 chosen feature which correlates with the severity of SCH. The
 CC expression and activity of the SFI, SPIs and related molecules (e.g.
 CC secondary messengers) are studied to diagnose SCH, monitor the progress
 CC of the disorder and the effectiveness of treatment and as targets to
 CC identify and produce potential therapeutic agents for the treatment of
 CC SCH. The paucity of detectable neuralgic defects distinguishes
 CC neuropsychiatric disorders such as SCH from neurological disorders, where
 CC manifestations of anatomical and biochemical changes have been identified
 CC in many cases. Consequently the identification and neuropathies are
 CC cellular and/or molecular causative defects and neuropathies are
 CC necessary for improved treatment of neuropsychiatric disorders. AAU1514-
 CC AAU1762 represent the amino acid sequences of schizophrenia-associated
 CC isoforms used in the method of the invention
 XX
 SQ Sequence 14 AA;
 SO
 QY Query Match 49.0%; Score 25; DB 4; Length 14;
 Best Local Similarity 80.0%; Pred. No. 9.8e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DB 2 FGYN 6
 9 FGYSN 13
 XX
 RESULT 39
 ABB52298
 ID ABB52298 standard; peptide; 14 AA.
 XX
 AC ABB52298;
 DT 08-FEB-2002 (first entry)
 XX
 DE Human APr-84 tryptic digest peptide #1.
 DE Human; neuroprotective; nootropic; gene therapy; vaccine;
 KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; APr;
 KW Alzheimer's Disease-Associated Protein Isoform; APr; tryptic digest;
 KW Expression Reference Protein Isoform; ERPI; proteolysis.
 XX
 OS Homo sapiens.
 PN WO200175454-A2.
 PD 11-OCT-2001.
 XX
 PF 03-APR-2001; 2001WO-US010908.
 XX

PR 03-APR-2000; 2000US-0194504P.
 PR 28-NOV-2000; 2000US-0253647P.
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 PA (PFIZ) PFIZER INC.
 XX
 XX
 PI Durham KL, Friedman DL, Herach HMC, Kimmel LH, Parekh RB;
 PI Porter DM, Rohlf C, Silber BW, Stiger TR, Sunderland PT;
 PI Townsend RR, White F, Williams SA;
 XX WPI; 2001-639384/73.
 DR
 PT Screening for Alzheimer's disease in a mammal, by making two-dimensional
 PT array of a feature whose relative abundance correlates with disease, and
 PT comparing with abundance of the feature in samples of healthy persons.
 PS Example; Page 32; 162pp; English.
 XX
 XX The invention relates to methods for the screening, diagnosis and
 CC prognosis of Alzheimer's disease. The methods involve the detection of
 CC Alzheimer's Disease-Associated Features (AFs) and Alzheimer's Disease-
 CC Associated Protein Isoforms (APIs) in cerebrospinal fluid, serum or
 CC plasma. The abundance of the AFs and APIs is then normalised to an
 CC Expression Reference Protein Isoform (ERPI) in order to determine whether
 CC a patient is suffering from, or has a predisposition to, Alzheimer's
 CC disease. The relative abundance of the AFs and APIs correlates with the
 CC severity of Alzheimer's Disease. The present sequence is a peptide
 CC produced from an API by proteolysis
 XX
 SQ Sequence 14 AA;
 XX
 Query Match 49.0%; Score 25; DB 4; Length 14;
 Best Local Similarity 80.0%; Pred. No. 9.8e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 FGYN 6
 DB 9 FGYSN 13
 XX
 RESULT 40
 ID AAE25488 standard; peptide; 14 AA.
 AC AAE25488;
 DT 30-OCT-2002 (first entry)
 DT 30-OCT-2002 (first entry)
 DE CAPI-19 tryptic peptide #2.
 XX Chronic asthma-associated protein isoform; CAPI; CAF; chronic asthma;
 KM chronic asthma-associated feature; screening; diagnosis; prognosis;
 KM tryptic peptide; therapy.
 XX
 XX Unidentified.
 OS
 XX WO200246768-A2.
 EN
 XX 13-JUN-2002.
 PD
 XX 10-DEC-2001; 2001WO-GB005476.
 PF
 XX 08-DEC-2000; 2000GB-00030051.
 PR
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 PA
 XX Hall IP, Terrett JA;
 PI
 XX WPI; 2002-537560/57.
 DR
 XX Screening chronic asthma by analyzing a test tissue sample by two
 PT dimensional electrophoresis to generate a two dimensional array of
 PT features and comparing the abundance of the test sample with a sample

PT free from chronic asthma.
 XX
 XX Disclosure; Page 25; 135pp; English.
 PS
 XX The invention relates to a method for screening, diagnosis or prognosis
 CC of chronic asthma using two dimensional electrophoresis to generate a two
 CC dimensional array of features. The invention also provides chronic asthma
 CC -associated protein isoforms (CAPIs) and chronic asthma-associated
 CC features (CAFs) detectable by two dimensional electrophoresis of tissue.
 CC The methods are useful for screening, diagnosis or prognosis of chronic
 CC asthma in a subject, for determining the stage or severity of chronic
 CC asthma, for identifying a subject at risk of developing chronic asthma,
 CC for monitoring the effect of therapy administered to a subject having
 CC chronic asthma and for treating or preventing asthma. They are also used
 CC for the manufacture of a medicament for the treatment or prevention of
 CC chronic asthma. The present sequence is CAPI tryptic peptide
 XX
 SQ Sequence 14 AA;
 XX
 Query Match 49.0%; Score 25; DB 5; Length 14;
 Best Local Similarity 80.0%; Pred. No. 9.8e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 FGYN 6
 DB 9 FGYSN 13
 XX
 RESULT 41
 ID ABJ15069 standard; peptide; 14 AA.
 AC ABJ15069;
 DT 10-DEC-2002 (first entry)
 DT 10-DEC-2002 (first entry)
 DE Human 125P5C8 epitope #3695.
 XX
 XX Human; 125P5C8; cancer; cytostatic; breast cancer; prostate cancer;
 KM bladder cancer; kidney cancer; colon cancer; ovarian cancer; epitope.
 KM
 XX Homo sapiens.
 OS
 XX WO200272785-A2.
 PN
 XX 19-SEP-2002.
 PD
 XX 13-MAR-2002; 2002MO-US007855.
 PF
 XX 14-MAR-2001; 2001US-00809638.
 PR
 XX (AGEN-) AGENSYS INC.
 PA
 XX Faris M, Challita-Zid PM, Hubert RS, Afar DEH, Ralciano AB, Ge W,
 PI Morrison RK, Morritson K, Jakobovits A;
 PI WPI; 2002-713510/77.
 DR
 XX New composition comprising a substance that modulates the status of
 PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for
 PT treating or preventing cancer that expresses or over expresses 125P5C8.
 PS Disclosure; Page 216; 274pp; English.
 XX
 XX The present invention relates to compositions comprising a substance that
 CC modulates the status of 125P5C8 or a molecule that is modulated by
 CC 125P5C8. The status of a cell that expresses 125P5C8 is modulated. The
 CC composition is useful for treating cancer, particularly prostate,
 CC bladder, kidney, colon, ovary or breast cancer. The 125P5C8 protein
 CC and/or a nucleotide sequence encoding the protein is useful for
 CC immunising a mammal against cancer. The present sequence is a 125P5C8
 CC epitope shown in the exemplification of the invention

SQ Sequence 14 AA;

Query Match 49.0%; Score 25; DB 5; Length 14;
 Best Local Similarity 44.4%; Pred. No. 9.8e+02;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 FGFKNSKE 9
 : : : : :
 DB 1 GHNVNTHF 9

RESULT 42

ABG67720

ID ABG67720 standard; peptide; 14 AA.

AC ABG67720;

DT 07-OCT-2002 (first entry)

DE Human ADPI tryptic digest peptide #429.

XX Human; Alzheimer's disease; AD; brain tissue; ADP; ADPI;

XX Alzheimer's disease-associated feature; neuroprotective;

XX Alzheimer's disease-associated protein isoform; nootropic;

XX ADPI tryptic digest peptide.

XX Homo sapiens.

XX WO200246767-A2.

XX 13-JUN-2002.

XX 29-NOV-2001; 2001WO-GB005289.

XX 08-DEC-2000; 2000US-0254431P.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX Herath HMAc, Parekh RB, Rohlf C;

XX WPI; 2002-508575/54.

Screening, diagnosis or prognosis of Alzheimer's disease in subject,
 PT comprising detecting Alzheimer disease-associated features or Alzheimer
 PT disease-associated protein isoforms in brain tissue from the subject.

PS Claim 7; Page 63; 427pp; English.

CC The present invention relates to methods and compositions for the
 CC screening, diagnosis or prognosis of Alzheimer's disease (AD) in a
 CC subject. The method comprises analysing a sample of brain tissue from a
 CC subject by 2D electrophoresis to generate a 2D array of Alzheimer's
 CC disease-associated features (ADPs), whose relative abundance correlates
 CC with the presence, absence, stage or severity of AD and comparing the
 CC abundance of each feature with the abundance of that chosen feature in
 CC brain tissue from persons free from AD. The invention also describes
 CC Alzheimer's disease-associated protein isoforms (ADPIs) detectable in
 CC brain tissue. The methods and compositions of the invention are useful
 CC for the screening, diagnosis or prognosis of AD in a subject, for
 CC determining the stage or severity of AD in a subject, for identifying a
 CC subject at risk of developing AD, or for monitoring the effect of therapy
 CC administered to a subject having AD. Antibodies capable of binding to
 CC ADPIs are useful for treating or preventing AD, and for determining the
 CC efficacy of a given treatment regime. An agent that modulates the
 CC activity of ADPI is useful in the manufacture of a medicament for the
 CC treatment or prevention of AD in a subject. ABG67292-ABG68038 represent
 CC human ADPI tryptic digest peptides

SQ Sequence 14 AA;

Query Match 49.0%; Score 25; DB 5; Length 14;
 Best Local Similarity 80.0%; Pred. No. 9.8e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 FGFKN 6
 : : : : :
 DB 9 FGKSN 13

RESULT 43

ABR91220

ID ABR91220 standard; peptide; 14 AA.

AC ABR91220;

DT 10-SEP-2003 (first entry)

DE P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:54.

XX Phlebotomus papatasi; salivary polypeptide; antigenic; immunogenic;

XX protozoacide; immunostimulant; vaccine; immune response; Leishmaniasis.

XX Synthetic.

XX WO2002102324-A2.

XX 27-DEC-2002.

XX 18-JUN-2002; 2002WO-US019663.

XX 19-JUN-2001; 2001US-0299391P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Valenzuela JG, Belkaid Y, Kamhawi S, Sacks D, Ribeiro JMC;

XX WPI; 2003-157000/15.

Novel isolated salivary polypeptide of Phlebotomus papatasi, useful for
 PT producing an immune response in a subject or for preventing Leishmaniasis
 PT in a subject.

PS Claim 10; Page 80; 279pp; English.

CC The present invention describes an isolated salivary polypeptide (I), of
 CC Phlebotomus papatasi. Also described: (1) an isolated nucleic acid (II)
 CC encoding (I); (2) an isolated fragment (III) of (II), where the fragment
 CC encodes the polypeptide fragment specific for a polypeptide such as
 CC Phlebotomus papatasi salivary polypeptide (PSP) 12, PSP14, PSP15,
 CC PSP30, PSP32, PSP36, PSP42 or PSP44; (3) an isolated antigenic or
 CC immunogenic fragment (IV) of (I); (4) a nucleic acid (V) that hybridises
 CC under stringent conditions to (II); (5) a vector (VI) comprising (II) or
 CC (III); and (6) a composition (VII) comprising (I) has protozoacide
 CC or (VII); and (6) a pharmaceutically acceptable carrier. (I) has protozoacide
 CC and immunostimulant activities, and can be used in vaccines. (VII) is
 CC useful for producing an immune response in a subject or for preventing
 CC Leishmaniasis in a subject. (II) is also useful for preventing
 CC Leishmaniasis in a subject. (VI) is useful as a vaccine. ACC79987 to
 CC ACC79999 and ABR91176 to ABR92046 represent sequences used in the
 CC exemplification of the present invention

SQ Sequence 14 AA;

Query Match 49.0%; Score 25; DB 6; Length 14;
 Best Local Similarity 37.5%; Pred. No. 9.8e+02;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 FGFKNSKE 9
 : : : : :
 DB 3 YGFANDKY 10

RESULT 44

ABR59105

ID ABR59105 standard; peptide; 14 AA.

XX ABR59105;
AC 11-JUL-2003 (first entry)
XX
XX Alzheimer's Disease-associated protein isoform, API-84, SEQ ID 240.
DE
XX Neotropic; Neuroprotective; Alzheimer's disease; API; human;
XX Alzheimer's Disease-associated protein isoform.
XX
XX Homo sapiens.
OS
XX WO2003028543-A2.
XX
XX 10-APR-2003.
XX
XX 03-OCT-2002; 2002WO-US031642.
XX
XX 03-OCT-2001; 2001US-0326708P.
XX
XX (Pfizer) Pfizer Prod Inc.
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
XX Durham LK, Friedman DJ, Herath HM, Kimmel LH, Parekh RB;
XX Potter DM, Rohlf C, Silber BM, Snyder PJ, Soares HD, Stiger TR;
XX Sunderland PT, Townsend RR, White WF, Williams SA;
XX MPI; 2003-371957/35.
XX
XX Screening or diagnosing of Alzheimer's disease (AD) determine the stage
XX or severity of AD in a subject, comprises analyzing a test sample of body
XX fluid from the subject by 2-dimensional electrophoresis.
XX
XX Claim 2; Page 50; 173pp; English.
XX
XX The present invention relates to methods for screening or diagnosing
XX Alzheimer's disease (AD) to determine the stage or severity of AD in a
XX subject, to identify subject at risk of developing AD, or to monitor the
XX effect of therapy administered. The methods comprise analysing a test
XX sample of body fluid by 2-dimensional electrophoresis to generate a 2-
XX dimensional array of AD-associated features (AFs). The method
XX alternatively comprises quantitatively detecting in a sample of body
XX fluid from the subject, one or more AD-associated protein isoforms (APIs;
XX ABR5710-ABR59184)
XX
XX Sequence 14 AA;
SQ

Query Match 49.0%; Score 25; DB 6; Length 14;
Best Local Similarity 80.0%; Pred. No. 9.8e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGYN 6
Db 9 FGYN 13

RESULT 45
ADA23853
ID ADA23853 standard; peptide; 14 AA.
XX
XX ADA23853;
XX
XX 20-NOV-2003 (first entry)
XX
XX Alzheimer's disease-associated protein isoform tryptic peptide #462.
DE
XX human; Alzheimer's disease; vascular dementia; Lewy body dementia;
XX schizophrenia; Parkinson's disease; multiple sclerosis; depression;
XX Alzheimer's disease-associated protein isoform; ADPI.
XX
XX Homo sapiens.
OS
XX
XX US2003064411-A1.
PN

XX 03-APR-2003.
PD
XX 10-DEC-2001; 2001US-00014340.
XX
XX 08-DEC-2000; 2000US-0254431P.
XX
XX (HERA/) HERATH H M A C.
XX (PARE/) PAREKH R B.
XX (ROHL/) ROHLF C.
XX
XX Herath HM, Parekh RB, Rohlf C;
XX MPI; 2003-540784/51.
XX
XX Screening, diagnosis or prognosis of Alzheimer's disease in subject,
XX involves analyzing test sample of brain tissue from subject, and
XX comparing feature in test sample with that of person(s) free from
XX Alzheimer's disease.
XX
XX Disclosure; SEQ ID NO 462; 115pp; English.
XX
XX The invention relates to a method of screening or diagnosing Alzheimer's
XX disease in a subject. The method is useful for screening, diagnosis or
XX prognosis of Alzheimer's disease in a subject for determining the stage
XX of severity of Alzheimer's disease in a subject, for identifying a
XX subject at risk of developing Alzheimer's disease, or for monitoring the
XX effect of therapy administered to a subject having Alzheimer's disease.
XX The method is also useful in treating vascular dementia, Lewy body
XX dementia, schizophrenia, Parkinson's disease, multiple sclerosis or
XX depression. The inventive method identifies sensitive and specific
XX biomarkers for the diagnosis of Alzheimer's disease in living subjects.
XX It provides therapeutic agents for Alzheimer's disease that works
XX quickly, potentially, specifically with fewer side effects. The present
XX sequence represents the amino acid sequence of a Alzheimer's disease-
XX associated protein isoform tryptic peptide.
XX
XX Sequence 14 AA;
SQ

Query Match 49.0%; Score 25; DB 6; Length 14;
Best Local Similarity 80.0%; Pred. No. 9.8e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGYN 6
Db 9 FGYN 13

Search completed: August 30, 2004, 10:49:28
Job time : 17.4088 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:34 ; Search time 10.5912 Seconds
(without alignments)
327.696 Million cell updates/sec

Title: US-09-720-469A-4
Perfect score: 60
Sequence: 1 GYKSKFHRVI 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 3347

Minimum DB seq length: 8

Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_todent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriopl:*
17: sp_archaeopl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	23	38.3	10	6	Q9TQV4
2	22	36.7	12	2	Q53579
3	22	36.7	12	4	Q8N6B2
4	22	36.7	13	3	P87031
5	21	35.0	12	11	Q8CJ30
6	20	33.3	14	4	Q9UNW6
7	20	33.3	14	12	Q56127
8	19	31.7	10	8	Q8HUB4
9	19	31.7	12	8	Q8HUB4
10	19	31.7	14	2	Q50268
11	18	30.0	10	6	Q9TQV3
12	18	30.0	11	7	Q78121
13	18	30.0	13	5	Q9TWM3
14	18	30.0	13	6	Q865C9
15	18	30.0	13	13	P82866
16	18	30.0	14	10	P82330

17	17	28.3	9	5	Q9TWX7	Q9TWX7 manduca sex
18	17	28.3	9	11	Q8CG13	Q8CG13 mus musculus
19	17	28.3	10	2	Q9X533	Q9X533 escherichia
20	17	28.3	10	2	Q9X534	Q9X534 leclercia a
21	17	28.3	11	10	Q941R5	Q941R5 pinus radia
22	17	28.3	12	6	Q9TJ31	Q9TJ31 callithrix
23	17	28.3	12	6	Q9TT29	Q9TT29 sagittus oe
24	17	28.3	13	2	Q47601	Q47601 escherichia
25	17	28.3	13	13	Q7Z2N6	Q7Z2N6 xenopus lae
26	17	28.3	14	12	Q53202	Q53202 porcine cit
27	16	26.7	8	2	Q4463	Q4463 rhizobiales
28	16	26.7	8	2	Q7X4C1	Q7X4C1 potato wite
29	16	26.7	8	13	Q8AWM0	Q8AWM0 coscoroba c
30	16	26.7	8	13	Q8AWM0	Q8AWM0 anser caeru
31	16	26.7	8	13	Q8AWM8	Q8AWM8 cygnus colu
32	16	26.7	8	13	Q8AWV7	Q8AWV7 anas platyr
33	16	26.7	9	8	Q8MEM3	Q8MEM3 howittia tr
34	16	26.7	10	12	Q86580	Q86580 simian para
35	16	26.7	11	8	Q8ME17	Q8ME17 sida hooker
36	16	26.7	11	8	Q8ME17	Q8ME17 sida hooker
37	16	26.7	11	8	Q8ME17	Q8ME17 sida hooker
38	16	26.7	11	8	Q8ME17	Q8ME17 sida hooker
39	16	26.7	11	8	Q8ME17	Q8ME17 sida hooker
40	16	26.7	11	8	Q8ME17	Q8ME17 sida hooker
41	16	26.7	11	8	Q8ME17	Q8ME17 sida hooker
42	16	26.7	11	8	Q8ME17	Q8ME17 sida hooker
43	16	26.7	11	8	Q8ME17	Q8ME17 sida hooker
44	16	26.7	11	8	Q8ME17	Q8ME17 sida hooker
45	16	26.7	11	8	Q8ME17	Q8ME17 sida hooker

ALIGNMENTS

RESULT 1
ID Q9TQV4 PRELIMINARY; PRT; 10 AA.
AC Q9TQV4
DT 01-MAY-2000 (TREMREL.13, Created)
DT 01-MAY-2000 (TREMREL.13, Last sequence update)
DT 01-JUN-2001 (TREMREL.17, Last annotation update)
DE POP-variant * transferin gene, EXON 17 and partial CDS (Fragment).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_Taxid=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Giffard J.M., Brandon R.B., Bell T.K.;
RT "Further identification of single nucleotide polymorphisms in the
RT equine transferrin gene."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF185778; AAF05491.1; -
DR EMBL; AF185770; AAF05483.1; -
DR EMBL; AF185772; AAF05484.1; -
DR EMBL; AF185771; AAF05485.1; -
DR EMBL; AF185773; AAF05486.1; -
DR EMBL; AF185774; AAF05487.1; -
DR EMBL; AF185775; AAF05488.1; -
DR EMBL; AF185776; AAF05489.1; -
DR EMBL; AF185777; AAF05490.1; -
FT NON FR
FT SEQUENCE 10 AA; 1188 MM; 6DF67DE9D1AEBDB CRC64;
Query Match 38.3%; Score 23; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 7 FHRV 10
Db 7 FHRV 10

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RESULT 2
ID 053579 PRELIMINARY; PRT; 12 AA.
AC 053579;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Light-harvesting complex I alpha polypeptide (Fragment).
CN PUF.
OS Rhodospirillum rubrum (Rhodospirillum rubrum).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Rhodospirillaceae; Rhodospirillum.
OC NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92234963; PubMed=1569029;
RA Richter P., Brand M., Drews G.;
RT "Characterization of LHT- and LHT+ Rhodospirillum rubrum mutants."
RT J. Bacteriol. 174:3030-3041(1992).
RL EMBL; S97551; AAC0405.1; -.
FT NON TER 12
SQ SEQUENCE 12 AA; 1627 MW; 0F92F6BA8A70532B CRC64;

Query Match
Best Local Similarity 36.7%; Score 22; DB 2; Length 12;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 SKFRV 10
DB 2 SKFYKI 7

RESULT 3
ID 08N6B2 PRELIMINARY; PRT; 12 AA.
AC 08N6B2;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Capacitative calcium channel protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=late pregnancy myometrium;
RX MEDLINE=22181008; PubMed=12193412;
RA Yang M., Gupta A., Shlykov S.G., Corrigan B., Tsujimoto S.,
RA Sanborn B.M.;
RT "Multiple rTP isoforms implicated in capacitative calcium entry are
RT expressed in human pregnant myometrium and myometrial cells."
RT Biol. Reprod. 67:988-994(2002).
RL EMBL; AF483645; AAM97860.1; -.
FT NON TER 12
SQ SEQUENCE 12 AA; 1511 MW; 4BF47B69BF1B5053 CRC64;

Query Match
Best Local Similarity 36.7%; Score 22; DB 4; Length 12;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYKSKFR 9
DB 1 GYENKIYK 9

RESULT 4
ID 087031 PRELIMINARY; PRT; 13 AA.
AC 087031;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

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DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE ORF YGR126W (Fragment).
OC Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OC NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Van Dyck L., Skala J., de Wergifosse P., Purnelle B., Talla E.,
RA Nawrocki A., Del Bino S., Goffeau A.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MIPS;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z72912; CAA97139.2; -.
FT NON TER 1
SQ SEQUENCE 13 AA; 1594 MW; 2954BA87F3F8C9C8 CRC64;

Query Match
Best Local Similarity 36.7%; Score 22; DB 3; Length 13;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 FHRV 10
DB 8 FHRI 11

RESULT 5
ID 08CJ30 PRELIMINARY; PRT; 12 AA.
AC 08CJ30;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myonectrin (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Kidney;
RX MEDLINE=20334280; PubMed=10873615;
RA Alliel P.M., Seddigi N., Goudou D., Cifuentes-Diaz C., Romero N.,
RA Velasco E., Rieger F., Perrin J.P.;
RT "Myonectrin, a novel member of the BTB/POZ-zinc finger family highly
RT expressed in human muscle."
RL Biochem. Biophys. Res. Commun. 273:385-391(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Kidney;
RA Bitoun M., Perrin J.P., Seddigi N., Goudou D., Camuzat A., Mattei M.G.,
RA Rieger F., Alliel P.M.;
RT "The human and mouse myonectrin genes: Genomic organization, splice
RT variants, chromosomal mapping and flanking genes."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF530457; AAN28710.1; -.
FT NON TER 1
SQ SEQUENCE 12 AA; 1448 MW; 5A48D26D6A331B3 CRC64;

Query Match
Best Local Similarity 35.0%; Score 21; DB 11; Length 12;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KNSKFR 9
DB 1 KNLKFKK 7

RESULT 6
ID 09UNM9

```

ID Q9UNM9 PRELIMINARY; PRT; 14 AA.
 AC Q9UNM9:
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE RING3 protein (Fragment).
 GN RING3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kedache M, Zhang F, Greenberg D.A.;
 RT "A Dinucleotide Repeat Between Exons 2 and 3 of the Human RING3
 Gene";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF107699; AAD24963.1; -;
 DR InterPro; IPR001487; Bromodomai.
 FT NON_TER 1 14
 FT NON_TER 1 14
 SQ SEQUENCE 14 AA; 1677 MW; 5CDDF036680AE22D3 CRC64;

Query Match 33.3%; Score 20; DB 4; Length 14;
 Best Local Similarity 40.0%; Pred. No. 6.9e+03;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 FRRVI 11
 :||:
 Db 2 YKXII 6

RESULT 7
 OS6127 PRELIMINARY; PRT; 14 AA.
 ID OS6127:
 AC OS6127:
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE ORF11.
 OS Porcine circovirus.
 OC Viruses; ssDNA viruses; Circoviridae; Circovirus.
 OC NCBI_TaxID=46221;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=pmw PCV;
 RX MEDLINE=98241772; PubMed=9573301;
 RA Hamel A.L., Lin L.L., Nayar G.P.;
 RT "Nucleotide sequence of porcine circovirus associated with postweaning
 RT multisystemic wasting syndrome in pigs";
 RL J. Virol. 72:5262-5267 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=pmw PCV;
 RA Hamel A.L., Lin L.L., Nayar G.P.S.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF021217; AAC59472.1; -;
 SQ SEQUENCE 14 AA; 1761 MW; 00F50DC89EBAF20B CRC64;

Query Match 33.3%; Score 20; DB 12; Length 14;
 Best Local Similarity 44.4%; Pred. No. 6.9e+03;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 KNSKFRHY 11
 :||:
 Db 2 KXKNHYEV 10

RESULT 8
 OS6127 PRELIMINARY; PRT; 10 AA.
 ID OS6127:
 AC OS6127:
 DT 01-MAR-2003 (TREMBlrel. 23, Created)

DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Ribosomal protein L16 (Fragment).
 GN RPL16.
 OS Anomobryum julaceum.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 OC Bryopsida; Bryidae; Bryales; Bryaceae; Anomobryum.
 OC NCBI_TaxID=67232;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AJ607;
 RA Pedersen N., Cox C., Hedenas L.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF546765; AAN62980.1; -;
 DR GO; GO:0009507; C:chloroplast; IEA.
 KM Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1326 MW; 6314C32409C321B4 CRC64;

Query Match 31.7%; Score 19; DB 8; Length 10;
 Best Local Similarity 42.9%; Pred. No. 7.6e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 KNSKFRH 9
 :||:
 Db 2 KRTKFRK 8

RESULT 9
 OS6127 PRELIMINARY; PRT; 12 AA.
 ID OS6127:
 AC OS6127:
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Ribosomal protein L16 (Fragment).
 GN RPL16.
 OS Bryum donianum.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 OC Bryopsida; Bryidae; Bryales; Bryaceae; Bryum.
 OC NCBI_TaxID=66993;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BD628;
 RA Pedersen N., Cox C., Hedenas L.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF546766; AAN63001.1; -;
 DR GO; GO:0009507; C:chloroplast; IEA.
 KM Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1539 MW; 5F27C314C32409C3 CRC64;

Query Match 31.7%; Score 19; DB 8; Length 12;
 Best Local Similarity 42.9%; Pred. No. 9.1e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 KNSKFRH 9
 :||:
 Db 2 KRTKFRK 8

RESULT 10
 OS6127 PRELIMINARY; PRT; 14 AA.
 ID OS6127:
 AC OS6127:
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-JAN-1999 (TREMBlrel. 09, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Rpl16 protein (Fragment).

GN RPL16.
 OS Phytoplasma sp.
 OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
 OC Acholeplasmataceae; Phytoplasma.
 ON NCBI_TaxID=2155;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lim P.-O., Sears B.B.;
 RT "DNA sequence of the ribosomal protein genes rpl2 and rpl9 from a
 RT plant-pathogenic mycoplasma-like organism.";
 RL FEBS Microbiol. Lett. 84:71-74(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92210505; PubMed=1556079;
 RA Lim P.-O., Sears B.B.;
 RT "Evolutionary relationships of a plant-pathogenic mycoplasma-like
 RT organism and Acholeplasma laidlawi deduced from two ribosomal protein
 RT gene sequences.";
 RL J. Bacteriol. 174:2606-2611(1992).
 DR EMBL; M74770; AAA2531.1; -.
 FT NON_TER
 SQ SEQUENCE 14 AA; 1870 MW; 87C315B73386A21 CRC64;

Query Match 31.7%; Score 19; DB 2; Length 14;
 Best Local Similarity 42.9%; Pred. No. 1.1e+04;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 KNSKFRH 9
 DB 5 KETKRR 11

RESULT 11
 ID Q9TJ33 PRELIMINARY; PRT; 10 AA.
 AC Q9TJ33
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE BRCA1 (Fragment).
 GN BRCA1.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 ON NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20154965; PubMed=10690375;
 RA Gray I.S., Yubasayan-Gurkan V.;
 RT "A single nucleotide (T-->G) polymorphism within intron 23 of the
 RT canine BRCA1 gene.";
 RL Anim. Gene. 31:76-77(2000).
 DR EMBL; AF159258; AAD56289.1; -.
 FT NON_TER
 SQ SEQUENCE 10 AA; 1164 MW; ZAB89C65BAA01B3 CRC64;

Query Match 30.0%; Score 18; DB 6; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 KNSKFRH 8
 DB 5 EDSGFH 10

RESULT 12
 ID 078121 PRELIMINARY; PRT; 11 AA.
 AC 078121;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE mhc class II B locus 12 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
 OC Cichlidae; Oreochromis.
 ON NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultman H., Klein U.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 RT class II B loci.";
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050027; AAC41366.1; -.
 FT NON_TER
 SQ SEQUENCE 11 AA; 1362 MW; 03C12D8EB7341B54 CRC64;

Query Match 30.0%; Score 18; DB 7; Length 11;
 Best Local Similarity 33.3%; Pred. No. 1.3e+04;
 Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 GYNSKFRH 9
 DB 1 GFMYRLSR 9

RESULT 13
 ID Q9TWM3 PRELIMINARY; PRT; 13 AA.
 AC Q9TWM3
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE LOCUSTAMYOINHIBIN, LOW-MH-MYOINHIBITING neuropeptide.
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelliatera; Acridomorpha;
 OC Acridoidea; Acrididae; Cerdipodinae; Locusta.
 ON NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=95063174; PubMed=7972937;
 RA Schoofs L., Veelaert D., Holman G.M., Hayes T.K., De Loof A.;
 RT "Partial identification, synthesis and immunolocalization of
 RT LocustamyoINHIBIN, the third myoinhibiting neuropeptide isolated from
 RT Locusta migratoria.";
 RL Regul. Pept. 52:139-156(1994).
 SQ SEQUENCE 13 AA; 1464 MW; D84ABBE624DC05A6 CRC64;

Query Match 30.0%; Score 18; DB 5; Length 13;
 Best Local Similarity 50.0%; Pred. No. 1.5e+04;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 KNSKFRH 10
 DB 5 KOSAFNAV 12

RESULT 14
 ID 0865C9 PRELIMINARY; PRT; 13 AA.
 AC 0865C9
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Glutamine synthetase (Fragment).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 ON NCBI_TaxID=9823;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Kim J.G., Vallet J.L., Christenson R.K.;
 RT "Characterization of porcine glutamine synthetase";
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY216477; AAC64254.1; -.
 FT NON-TER
 SQ SEQUENCE 13 AA; 1555 MW; 87987A0B71AB6B1A CRC64;

Query Match 30.0%; Score 18; DB 6; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YRN 4
 DB 11 YRN 13

RESULT 15
 P82866 PRELIMINARY; PRT; 13 AA.

AC P82866;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE RNA-binding protein (Fragment).
 OS Rana pipiens (Northern leopard frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8404;
 RN [1]
 RP SEQUENCE.
 RC Tissue-Embryonic epithelium;
 RA Banerjee H.N., Blackmon R.H., Moses A., Harmon G.L., Peterson B.L.,
 RA Khan A.;
 RT "Isolation, identification and characterization of a novel 5'UTR
 binding protein for VCAM-1";
 RL Submitted (NOV-2000) to Swiss-Prot.
 CC -1- FUNCTION: BINDS TO THE VCAM-1 5'UTR REGION.
 CC -1- SIMILARITY: TO THE FETUIN FAMILY.
 CC PIR; A59387; A59387.
 DR GO; GO:0003723; rRNA binding; IEA.
 DR InterPro; IPR001363; Fetuin.
 DR PROSITE; PS01254; FETUIN_1; PARTIAL.
 DR PROSITE; PS01255; FETUIN_2; PARTIAL.
 KW RNA-binding.
 FT NON-TER
 SQ SEQUENCE 13 AA; 1370 MW; C683612A61757DC2 CRC64;

Query Match 30.0%; Score 18; DB 13; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYK 3
 DB 8 GYK 10

RESULT 16
 P82330 PRELIMINARY; PRT; 14 AA.

AC P82330;
 DT 01-JUN-2000 (TREMBlrel. 14, Created)
 DT 01-JUN-2000 (TREMBlrel. 14, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Unknown protein from 2D-page of thylakoid PERIPHERY (SPOT112)
 DE (Fragment).
 OS Pisum sativum (Garden pea).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
 OX NCBI_TaxID=3888;
 RN [1]

RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
 RC STRAIN=cv. DE GRACE; TISSUE=LEAF;
 RX MEDLINE=20181728; PubMed=10715320;
 RA Peltier J.-B., Friso G., Kalame D.E., Roepstorff P., Nilsson F.,
 RA Adamska I., van Wijk K.J.;
 RT "Proteomics of the chloroplast: systematic identification and
 targeting analysis of lumenal and peripheral thylakoid proteins";
 RL Plant Cell 12:319-341(2000).
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE PERIPHERY.
 CC -1- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 PROTEIN IS: 6, ITS MW IS: 22.9 KDA.
 DR GO; GO:0009587; C:chloroplast; IEA.
 DR GO; GO:0009579; C:thylakoid; IEA.
 KW Chloroplast; Thylakoid.
 FT NON-TER
 SQ SEQUENCE 14 AA; 1405 MW; 8051E964D580014A CRC64;

Query Match 30.0%; Score 18; DB 10; Length 14;
 Best Local Similarity 44.4%; Pred. No. 1.6e+04;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 KNSKFRFVI 11
 DB 3 KGSDDNRVL 11

RESULT 17
 Q9TWMX7 PRELIMINARY; PRT; 9 AA.

AC Q9TWMX7;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Juvenile hormone binding protein, JHBP=4.9 kDa GUV-C peptide
 DE (Fragment).
 OS Manduca sexta (tobacco hawkmoth) (tobacco hornworm).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
 CC Sphingidae; Sphinginae; Manduca.
 OX NCBI_TaxID=7130;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92134256; PubMed=1734862;
 RA Toubara K., Prestwich G.D.;
 RT "Binding site mapping of a photoaffinity-labeled juvenile hormone
 binding protein";
 RL Biochem. Biophys. Res. Commun. 182:466-473(1992).
 FT NON-TER
 SQ SEQUENCE 9 AA; 1023 MW; E063C40045A2D401 CRC64;

Query Match 28.3%; Score 17; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 HRV 10
 DB 2 HRV 4

RESULT 18
 Q8CG13 PRELIMINARY; PRT; 9 AA.

AC Q8CG13;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Glutamate receptor ionotropic N-methyl D-aspartate-like 1A
 DE (Fragment).
 GN GRIN1A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RA Wyder K.S., Mohan Raj B.K., Sciorra L.J., Roginski R.S.;
 RT "The mouse orthologue of the human ionotropic glutamate receptor-1-like
 gene (GRIN1A) maps to mouse chromosome 9."
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF462417; AAO15648.1;
 DR EMBL; AF462416; AAO15648.1; JOINED.
 DR MGD; MGI:107282; Grin1a.
 KW GO; GO:0004872; F:receptor activity; IEA.
 KM Receptor.
 FT NON_TER 1
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1091 MW; 6A91233EB059C33B CRC64;
 Query Match 28.3%; Score 17; DB 11; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1e+06; 1; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 NSKF 7
 DB 1 NEKF 4
 RESULT 19
 ID Q9X533 PRELIMINARY; PRT; 10 AA.
 AC Q9X533;
 DT 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Periplasmic mercuroic ion binding protein (Fragment).
 GN MERP.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=209A;
 RX MEDLINE=97208220; PubMed=9055422;
 RA Liebert C.A., Wireman J., Smith T., Summers A.O.;
 RT "Phylogeny of mercury resistance (mer) operons of gram-negative
 bacteria isolated from the fecal flora of primates."
 RL Appl. Environ. Microbiol. 63:1066-1076 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=209A;
 RX MEDLINE=98027386; PubMed=9361435;
 RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
 RT "Association of mercury resistance with antibiotic resistance in the
 gram-negative fecal bacteria of primates."
 RL Appl. Environ. Microbiol. 63:4494-4503 (1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=209A;
 RX MEDLINE=20568355; PubMed=1116334;
 RA Liebert C.A., Watson A.L., Summers A.O.;
 RT "The quality of merC, a module of the mer mosaic."
 RL J. Mol. Evol. 51:607-622 (2000).
 DR EMBL; AF120964; AAD23785.1; -.
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1093 MW; 3F526335A5A77B58 CRC64;
 Query Match 28.3%; Score 17; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.8e+04; 1; Indels 0; Gaps 0;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GYKNS 5
 DB 1 NEKF 4

DB 3 GTPSS 7
 RESULT 20
 ID Q9X534 PRELIMINARY; PRT; 10 AA.
 AC Q9X534;
 DT 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Periplasmic mercuroic ion binding protein (Fragment).
 GN MERP.
 OS Lacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Lacteria.
 OX NCBI_TaxID=83655;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=742H;
 RX MEDLINE=97208220; PubMed=9055422;
 RA Liebert C.A., Wireman J., Smith T., Summers A.O.;
 RT "Phylogeny of mercury resistance (mer) operons of gram-negative
 bacteria isolated from the fecal flora of primates."
 RL Appl. Environ. Microbiol. 63:1066-1076 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=742H;
 RX MEDLINE=98027386; PubMed=9361435;
 RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
 RT "Association of mercury resistance with antibiotic resistance in the
 gram-negative fecal bacteria of primates."
 RL Appl. Environ. Microbiol. 63:4494-4503 (1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=742H;
 RX MEDLINE=20568355; PubMed=1116334;
 RA Liebert C.A., Watson A.L., Summers A.O.;
 RT "The quality of merC, a module of the mer mosaic."
 RL J. Mol. Evol. 51:607-622 (2000).
 DR EMBL; AF120965; AAD23785.1; -.
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1093 MW; 3F526335A5A77B58 CRC64;
 Query Match 28.3%; Score 17; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.8e+04; 1; Indels 0; Gaps 0;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GYKNS 5
 DB 3 GTPSS 7
 RESULT 21
 ID Q94IRS PRELIMINARY; PRT; 11 AA.
 AC Q94IRS;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Nonspecific lipid transfer protein (Fragment).
 OS Pinus radiata (Monterey pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Serrnatoophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=3347;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PRLP9-1158055;
 RA Jones D.F.;
 RT "Genetic mapping of the lipid transfer protein gene family in Pinus
 radiata and Pinus taeda."
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY029028; AAK40266.1; -.
 FT NON_TER 11

SEQ SEQUENCE 11 AA; 1361 MW; 471B518D473AE727 CRC64;

Query Match 28.3%; Score 17; DB 10; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.9e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NSKF 7
DB 8 NSQF 11

RESULT 22

Q9TT31 PRELIMINARY; PRT; 12 AA.
AC Q9TT31; 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Beta-globin (Fragment).
OS Callitrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callitrix.
CX NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=20188601; PubMed=10723742;
RA Francisco M.P., Ochman H.;
RT "Strand Symmetry around the beta-globin Origin of Replication in
RT Primates";
RL Mol. Biol. Evol. 17:416-422(2000).
DR EMBL; AF205413; AAF23764.1; --
FT NON_TER
SQ SEQUENCE 12 AA; 1251 MW; 07BC8FAE8D72DD4 CRC64;

Query Match 28.3%; Score 17; DB 6; Length 12;
Best Local Similarity 33.3%; Pred. No. 2.1e+04;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 GYKSKFHR 9
DB 2 GVANALAHK 10

RESULT 23

Q9TT29 PRELIMINARY; PRT; 12 AA.
AC Q9TT29; 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Beta-globin (Fragment).
OS Saginus oedipus (Cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saginus.
CX NCBI_TaxID=9490;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=20188601; PubMed=10723742;
RA Francisco M.P., Ochman H.;
RT "Strand Symmetry around the beta-globin Origin of Replication in
RT Primates";
RL Mol. Biol. Evol. 17:416-422(2000).
DR EMBL; AF205415; AAF23766.1; --
FT NON_TER
SQ SEQUENCE 12 AA; 1251 MW; 07BC8FAE8D72DD4 CRC64;

Query Match 28.3%; Score 17; DB 6; Length 12;
Best Local Similarity 33.3%; Pred. No. 2.1e+04;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 GYKSKFHR 9

DB 2 GVANALAHK 10

RESULT 24

Q47601 PRELIMINARY; PRT; 13 AA.
AC Q47601; 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE C (Fragment).
GN C.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
CX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91139577; PubMed=1995588;
RA Tao T., Bourne J.C., Blumenthal R.M.;
RT "A family of regulatory genes associated with type II restriction-
RT modification systems";
RL J. Bacteriol. 173:1367-1375(1991).
DR EMBL; M63620; AAA24557.1; --
FT NON_TER
SQ SEQUENCE 13 AA; 1485 MW; DABCB13667902866 CRC64;

Query Match 28.3%; Score 17; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.3e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYKSK 6
DB 7 GLKNEQ 12

RESULT 25

Q7ZZN6 PRELIMINARY; PRT; 13 AA.
AC Q7ZZN6; 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Zinc finger protein (Fragment).
GN ZIC3.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus.
CX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum;
RA Weber J.R., Sokol S.Y.;
RT "Identification of a phylogenetically conserved activin-responsive
RT enhancer in the Zic3 gene";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF506278; AAP20809.1; --
FT NON_TER
SQ SEQUENCE 13 AA; 1537 MW; 5DDA56257F6DF2C3 CRC64;

Query Match 28.3%; Score 17; DB 13; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.3e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KNSKF 8
DB 3 KHKVH 8

RESULT 26

093202
ID 093202 PRELIMINARY; PRT; 14 AA.
AC 093202; Q9YJ34;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE ORF1.
OS Porcine circovirus,
OS Porcine circovirus type 2-D,
OS Porcine circovirus type 2-C,
OS Porcine circovirus type 2-B,
OS Porcine circovirus type 2-B,
OS Bovine circovirus, and
OS Porcine circovirus type 2.
OC Viruses; ssDNA viruses; Circoviridae; Circovirus.
NCBI_TaxID=46221, 86385, 85543, 85544, 85709, 85542, 85708;
[1]
RP SEQUENCE FROM N.A.
RC SPECIES=porcine circovirus; STRAIN=PORCINE CIRCOVIRUS TYPE II;
RX MEDLINE=98418498; PubMed=9747726;
RA Meenan B.M., McNeill P.M., Todd D., Kennedy S., Jewhurst V.,
Ralls J.A., Hesser L.E., Clark E.G., Haines D.M., Allan G.M.,
RT "Characterization of novel circovirus DNAs associated with wasting
syndromes in pigs."
J. Gen. Virol. 79:2171-2199 (1998).
[2]
RP SEQUENCE FROM N.A.
RC SPECIES=porcine circovirus; STRAIN=PORCINE CIRCOVIRUS TYPE II;
RA Meenan B.M.,
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RC SPECIES=porcine circovirus type 2-D;
RA Hamel A.L., Nayar G.P.S.;
RT "Genetic characterization of four novel type-2 Porcine circoviruses."
Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RC SPECIES=porcine circovirus type 2-C, and porcine circovirus type 2-E;
RA Hamel A.L., Nayar G.P.S.;
RT "Nucleotide sequence of four different isolates of circovirus detected
in pigs with various clinical syndromes."
Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE FROM N.A.
RC SPECIES=porcine circovirus type 2-B;
RA Hamel A.L., Nayar G.P.S.;
RT "Nucleotide sequence of four different isolates of porcine circovirus
detected in pigs with various clinical syndromes."
Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
[6]
RP SEQUENCE FROM N.A.
RC SPECIES=bovine circovirus;
RA Hamel A.L., Nayar G.P.S.;
RT "Nucleotide sequence of a circovirus detected in cattle with various
clinical syndromes."
Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
[7]
RP SEQUENCE FROM N.A.
RC SPECIES=porcine circovirus type 2; STRAIN=24657 NT;
RA Wellenberg G.J., Pesch S., Berendsen P.M., Steyerink P.J.G.M.,
Hunnen W., Van der Vorst T.J.K., Peperkamp N.H.M.T., Ohlinger V.F.,
Schippers R., Van Oirschot J.T., de Jong M.F.;
RT "Isolation and characterization of porcine circovirus type 2 from pigs
showing signs of post-weaning multisystemic wasting syndrome in The
Netherlands."
Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF055394; AAC35336.1; -
DR EMBL: AF055391; AAC35305.1; -
DR EMBL: AF055392; AAC35316.1; -
DR EMBL: AF055393; AAC35326.1; -
DR EMBL: AF117753; AAD12313.1; -
DR EMBL: AF109398; AAD03069.1; -

DR EMBL: AF109399; AAD03080.1; -
DR EMBL: AF12862; AAD03090.1; -
DR EMBL: AF109397; AAD11937.1; -
DR EMBL: AF201897; AAG41230.1; -
SO SEQUENCE 14 AA; 1747 MW; 00F50DC89AEFF20B CRC64;
Query Match
Best Local Similarity 28.3%; Score 17; DB 12; Length 14;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 4 NSKFH 8
Db 2 NKNH 6
RESULT 27
ID Q4463 PRELIMINARY; PRT; 8 AA.
AC Q4463;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Agrobacterium tumefaciens Ti plasmid virD3 and virD4 genes
DE (fragment).
OS Rhizobiales (rhizobacteria).
OC Bacteria; Proteobacteria; Alphaproteobacteria.
NCBI_TaxID=356;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8015611; PubMed=3658701;
RA Portner S.G., Yanofsky M.F., Nester E.W.;
RT "Molecular characterization of the virD operon from Agrobacterium
tumefaciens."
J. Nucleic Acids Res. 15:7503-7517 (1987).
DR EMBL: X06045; CAA29439.1; -
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
FT NON TER
SQ SEQUENCE 8 AA; 887 MW; F8F2C325B33861A6 CRC64;
Query Match
Best Local Similarity 26.7%; Score 16; DB 2; Length 8;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 SKFH 8
Db 5 SKVH 8
RESULT 28
ID Q7X4C1 PRELIMINARY; PRT; 8 AA.
AC Q7X4C1;
DT 01-OCT-2003 (TREMblrel. 25, Created)
DT 01-OCT-2003 (TREMblrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Ribosomal protein S19 (fragment).
GN RPS19.
OS Potato witches'-broom phytoplasma.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmales;
OC Acholeplasmataceae; Phytoplasma.
NCBI_TaxID=37701;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=PWB;
RA Lee I.-M., Martini M., Marcone C., Zhu S.;
RT "Classification of phytoplasma strains in the elm yellows group
(16S rV) and proposition of 'Candidatus Phytoplasma ulmi' for the
phytoplasma associated with elm yellows and 'Candidatus Phytoplasma
chinese' for the phytoplasma associated with cherry lethal yellowing
in China."
Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY197682; AAP42406.1; -.
 KW Ribosomal protein.
 FT NON TER 1
 SQ SEQUENCE 8 AA; 945 MW; 783326D443333AA8 CRC64;

Query Match 26.7%; Score 16; DB 2; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1e+06;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 KMSK 6
 DB 4 KMSK 7

RESULT 29

Q8AWM0 PRELIMINARY; PRT; 8 AA.
 AC Q8AWM0; 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 GN LDH-B (Fragment).
 OS Coscoroba coscoroba (Coscoroba swan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Coscoroba.
 OX NCBI_TaxID=8863;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cotter J.-P., StJohn J., Quinn T.W.;
 RT "Isolation of a Precisely Delineated, Recently Transposed Chicken
 Repeat 1 (CR1) Retrotransposon Within an Intron of the Coscoroba
 coscoroba.";
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY123324; AAM96899.1; -.
 FT NON TER 1
 FT NON TER 8
 SQ SEQUENCE 8 AA; 911 MW; D73AADC2C05331F1 CRC64;

Query Match 26.7%; Score 16; DB 13; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1e+06;
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 HRVI 11
 DB 2 HKIV 5

RESULT 30

Q8AWV9 PRELIMINARY; PRT; 8 AA.
 AC Q8AWV9; 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 GN LDH-B (Fragment).
 OS Anser caerulescens caerulescens (snow goose).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anser.
 OX NCBI_TaxID=70340;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cotter J.-P., StJohn J., Quinn T.W.;
 RT "Isolation of a Precisely Delineated, Recently Transposed Chicken
 Repeat 1 (CR1) Retrotransposon Within an Intron of the Coscoroba
 coscoroba.";
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY123325; AAM96899.1; -.
 FT NON TER 1
 FT NON TER 8
 SQ SEQUENCE 8 AA; 911 MW; D73AADC2C05331F1 CRC64;

Query Match 26.7%; Score 16; DB 13; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1e+06;
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 HRVI 11
 DB 2 HKIV 5

RESULT 31

Q8AWV8 PRELIMINARY; PRT; 8 AA.
 AC Q8AWV8; 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 GN LDH-B (Fragment).
 OS Cygnus columbianus (tundra swan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Cygnus.
 OX NCBI_TaxID=110926;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cotter J.-P., StJohn J., Quinn T.W.;
 RT "Isolation of a Precisely Delineated, Recently Transposed Chicken
 Repeat 1 (CR1) Retrotransposon Within an Intron of the Coscoroba
 coscoroba.";
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY123326; AAM96900.1; -.
 FT NON TER 1
 FT NON TER 8
 SQ SEQUENCE 8 AA; 911 MW; D73AADC2C05331F1 CRC64;

Query Match 26.7%; Score 16; DB 13; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1e+06;
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 HRVI 11
 DB 2 HKIV 5

RESULT 32

Q8AWV7 PRELIMINARY; PRT; 8 AA.
 AC Q8AWV7; 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 GN LDH-B (Fragment).
 OS Anas platyrhynchos (Domestic duck).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
 OX NCBI_TaxID=8839;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cotter J.-P., StJohn J., Quinn T.W.;
 RT "Isolation of a Precisely Delineated, Recently Transposed Chicken
 Repeat 1 (CR1) Retrotransposon Within an Intron of the Coscoroba
 coscoroba.";
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY123327; AAM96901.1; -.
 FT NON TER 1
 FT NON TER 8
 SQ SEQUENCE 8 AA; 911 MW; D73AADC2C05331F1 CRC64;

Query Match 26.7%; Score 16; DB 13; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1e+06;
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 HRVI 11

DB 2 HKIV 5

RESULT 33

OC MEM3 PRELIMINARY; PRT; 9 AA.

DT 01-OCT-2002 (TRENBLREL. 22, Created)
DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Howittia trilobularis.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids 1; Malvales; Malvaceae; Malvoideae; Howittia.
OX NCBI_TaxID=183272;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of ndhF and the rpl16 intron."
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384615; AAM50387.1; -
DR GO; GO:0009507; C:chloroplast; IEA.
KM Chloroplast.
FT NON TER 1 1
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1256 MW; 6351D32409D411B4 CRC64;

Query Match 26.7%; Score 16; DB 8; Length 9;
Best Local Similarity 28.6%; Pred. No. 1e+06;
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 KNSKFR 9
DB 1 KRTFRK 7

RESULT 34

OC MEM3 PRELIMINARY; PRT; 10 AA.

DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-NOV-1996 (TRENBLREL. 08, Last annotation update)
DE Large protein (Fragment).
OS Simian parainfluenza virus 5.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OC NCBI_TaxID=11207;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93224905; PubMed=8385701;
RA Higuchi Y., Miyahara Y., Kawano M., Tsurudome M., Matsumura H.,
RA Kusagawa S., Komada H., Nishio M., Ito Y.;
RT "Sequence analysis of the large (L) protein of simian virus 5."
RL J. Gen. Virol. 74:789-789(1993).
DR EMBL; S57860; AAB26118.1; -
FT NON TER 1 1
FT NON TER 1 1
SQ SEQUENCE 10 AA; 1144 MW; 0C25A0D3C86776D4 CRC64;

Query Match 26.7%; Score 16; DB 12; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.7e+04;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYKN 4
DB 6 GRON 9

RESULT 35

OC MEM3 PRELIMINARY; PRT; 11 AA.

DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLREL. 14, Last annotation update)
DE Heat shock protein 60 homolog (Fragment).
OS Pichia angusta (Yeast) (Hansenula polymorpha).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.
OX NCBI_TaxID=4905;
RN [1]
RP SEQUENCE.
RA Evers M.E., Hubbe B., Titorenko V.I., Kunau W.H., Hartl F.U.,
RA Harder W., Veenhuis M.;
RT "Affinity purification of molecular chaperones of the yeast Hansenula
RT polymorpha using immobilized denatured alcohol oxidase."
RL FEBS Lett. 321:32-36(1993).
SQ SEQUENCE 11 AA; 1230 MW; 71872C1779C3372B CRC64;

Query Match 26.7%; Score 16; DB 3; Length 11;
Best Local Similarity 50.0%; Pred. No. 3e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YNSKF 7
DB 2 HKELKF 7

RESULT 36

OC MEM3 PRELIMINARY; PRT; 11 AA.

DT 01-OCT-2002 (TRENBLREL. 22, Created)
DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Sida hookeriana.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids 1; Malvales; Malvaceae; Malvoideae; Sida.
OX NCBI_TaxID=108446;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of ndhF and the rpl16 intron."
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384624; AAM50396.1; -
DR GO; GO:0009507; C:chloroplast; IEA.
KM Chloroplast.
FT NON TER 1 1
FT NON TER 1 1
FT NON TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 26.7%; Score 16; DB 8; Length 11;
Best Local Similarity 28.6%; Pred. No. 3e+04;
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 KNSKFR 9
DB 1 KRTFRK 7

RESULT 37

OC MEM3 PRELIMINARY; PRT; 11 AA.

DT 01-OCT-2002 (TRENBLREL. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Lagunaria patersonia.
 OG Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC eurosids II; Malvales; Malvaceae; Malvoideae; Lagunaria.
 OC NCBI_TaxID=183274;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron."
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384616; AAM50388.1; -;
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 26.7%; Score 16; DB 8; Length 11;
 Best Local Similarity 28.6%; Pred. No. 3e+04;
 Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 KNSKFSR 9
 DB 1 KRTRFRK 7

RESULT 38
 Q8ME55 PRELIMINARY; PRT; 11 AA.
 AC Q8ME55.
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Abolmoschus manihot.
 OG Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC eurosids II; Malvales; Malvaceae; Malvoideae; Abelmoschus.
 OC NCBI_TaxID=183220;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron."
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384561; AAM50399.1; -;
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 26.7%; Score 16; DB 8; Length 11;
 Best Local Similarity 28.6%; Pred. No. 3e+04;
 Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 KNSKFSR 9
 DB 1 KRTRFRK 7

RESULT 39
 Q8ME50 PRELIMINARY; PRT; 11 AA.
 ID Q8ME50.
 AC Q8ME50;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Hibiscus peralbus.
 OG Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
 OC NCBI_TaxID=183256;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron."
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384598; AAM50370.1; -;
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 26.7%; Score 16; DB 8; Length 11;
 Best Local Similarity 28.6%; Pred. No. 3e+04;
 Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 KNSKFSR 9
 DB 1 KRTRFRK 7

RESULT 40
 Q8ME51 PRELIMINARY; PRT; 11 AA.
 AC Q8ME51.
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Alyogyne pinoniana.
 OG Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC eurosids II; Malvales; Malvaceae; Malvoideae; Alyogyne.
 OC NCBI_TaxID=183226;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron."
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384566; AAM50404.1; -;
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 26.7%; Score 16; DB 8; Length 11;
 Best Local Similarity 28.6%; Pred. No. 3e+04;
 Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 KNSKFSR 9
 DB 1 KRTRFRK 7

RESULT 41
 Q8MEP3 PRELIMINARY; PRT; 11 AA.
 ID Q8MEP3.
 AC Q8MEP3;

AC Q8MEP3;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Hibiscus normanii.
 OC Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC eucosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
 OX NCBI_TaxID=183253;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384595; AAM50367.1; -
 DR GO; GO:0009507; C:chloroplast; IEA.
 KM Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 26.7%; Score 16; DB 8; Length 11;
 Best Local Similarity 28.6%; Pred. No. 3e+04;
 Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 KNSKFR 9
 | : : | :
 1 KRTFRK 7

RESULT 42

ID Q8MEQ7 PRELIMINARY; PRT; 11 AA.
 AC Q8MEQ7;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Hibiscus drummondii.
 OC Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC eucosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
 OX NCBI_TaxID=183239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384581; AAM50353.1; -
 DR GO; GO:0009507; C:chloroplast; IEA.
 KM Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 26.7%; Score 16; DB 8; Length 11;
 Best Local Similarity 28.6%; Pred. No. 3e+04;
 Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 KNSKFR 9
 | : : | :
 1 KRTFRK 7

RESULT 43

Q8MEL9

ID Q8MEL9 PRELIMINARY; PRT; 11 AA.
 AC Q8MEL9;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Pavonia hastata.
 OC Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC eucosids II; Malvales; Malvaceae; Malvoideae; Pavonia.
 OX NCBI_TaxID=183278;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384622; AAM50394.1; -
 DR GO; GO:0009507; C:chloroplast; IEA.
 KM Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 26.7%; Score 16; DB 8; Length 11;
 Best Local Similarity 28.6%; Pred. No. 3e+04;
 Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 KNSKFR 9
 | : : | :
 1 KRTFRK 7

RESULT 44

ID Q8MERO PRELIMINARY; PRT; 11 AA.
 AC Q8MERO;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Hibiscus coatesii.
 OC Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC eucosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
 OX NCBI_TaxID=183236;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384578; AAM50416.1; -
 DR GO; GO:0009507; C:chloroplast; IEA.
 KM Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 26.7%; Score 16; DB 8; Length 11;
 Best Local Similarity 28.6%; Pred. No. 3e+04;
 Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 KNSKFR 9
 | : : | :
 1 KRTFRK 7

RESULT 45

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Q8MES3
ID Q8MES3 PRELIMINARY; PRT; 11 AA.
AC Q8MES3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Alyogyne cravenii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Malvales; Malvaceae; Malvoideae; Alyogyne.
OX NCBI_TaxID=183223;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
RL Syst. Bot. 27:333-350 (2002).
DR EMBL: AF384563; RAM50401.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 26.7%; Score 16; DB 8; Length 11;
Best Local Similarity 28.6%; Pred. No. 3e+04;
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 KNSKTFHR 9
|::|:
Db 1 KRTRFRX 7

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Search completed: August 30, 2004, 10:55:18
 Job time : 12.5912 secs


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DE 28-FEB-2003 (Rel. 41, last annotation update)
DE FMRFamide-like neuropeptide FLP7 (GYRKPFPNGSIF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sitihinggorngul P., Pupum J., Krungrasem C., Longyant S.,
RA Sitihinggorngul P., Sitihinggorngul W., Petsom A.;
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon."
RL Comp. Biochem. Physiol. 133B:325-337(2002).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1381.4; METHOD=MALDI.
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
DR GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD_RES 12 AA; 1383 MW; 31209192EF49D777 CRC64;
SQ SEQUENCE 12 AA; 1383 MW; 31209192EF49D777 CRC64;

Query Match 33.3%; Score 20; DB 1; Length 12;
Best Local Similarity 37.5%; Pred. No. 5.7e+02;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYKSKPF 8
DB 1 GYRKPFPN 8

RESULT 3
ID TMA1_LOCMT STANDARD; PRT; 13 AA.
AC P38496;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Lom-AG-mycotropin I (Accessory gland myotropin I).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preyrgota;
OC Neoptera; Orthoptera; Orthoptera; Caelifera; Acridoidea;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Male accessory gland.
RX MEDLINE=91271087; PubMed=2052501;
RA Paemen L., Lips A., Schoofs L., Proost P., Van Damme J., de Loof A.;
RT "Lom-AG-mycotropin: a novel myotropic peptide from the male accessory
RT glands of Locusta migratoria."
RL Peptides 12:7-10(1991).
CC -1- FUNCTION: The exact physiological function is still unknown. This
CC myotropic peptide is active on the oviduct and, to a lesser
CC extent, on the hindgut. Transferred from the male to the female
CC during copulation.
CC -1- TISSUE SPECIFICITY: Male accessory glands.
KW Neuropeptide; Amidation.
FT MOD_RES 13 AA; 1368 MW; DELACAPC482EB72D CRC64;
SQ SEQUENCE 13 AA; 1368 MW; DELACAPC482EB72D CRC64;

Query Match 33.3%; Score 20; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 6.2e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYKXN 4
DB 1 GYKXN 4

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RESULT 4
ID COXG_RAT STANDARD; PRT; 8 AA.
AC P60430;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, last annotation update)
DE Cytochrome c oxidase polypeptide VIIb (EC 1.9.3.1) (AED) (Fragment).
OS COX6B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=95334529; PubMed=7601105;
RA Schaeffer H., Noack H., Halenka W., Brandt U., von Jagow G.;
RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
RT amino-terminal sequences suggest identity of the fetal heart and the
RT adult liver isoform."
RL Eur. J. Biochem. 230:235-241(1995).
CC -1- FUNCTION: This protein is one of the nuclear-coded polypeptide
CC chains of cytochrome c oxidase, the terminal oxidase in
CC mitochondrial electron transport. This protein may be one of the
CC heme-binding subunits of the oxidase.
CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -1- SIMILARITY: Belongs to the cytochrome c oxidase VIIb family.
DR PIR: S65381; S65381.
KW Oxidoreductase; Mitochondrion.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 1039 MW; 8101E9CA73AE456 CRC64;

Query Match 31.7%; Score 19; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 FHR 9
DB 6 FHR 8

RESULT 5
ID FAP7_MACRS STANDARD; PRT; 10 AA.
AC P83280;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLP7 (GYGDRNRLRF-amide).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21107394; PubMed=11179812;
RA Sitihinggorngul P., Sarathongkum W., Longyant S., Panchan N.,
RA Sitihinggorngul W., Petsom A.;
RT "Three more novel FMRFamide-like neuropeptide sequences from the
RT eyestalk of the giant freshwater prawn Macrobrachium rosenbergii."
RL Peptides 22:191-197(2001).
CC -1- MASS SPECTROMETRY: MW=1244.9; METHOD=MALDI.
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
DR GO:0007218; P:neuropeptide signaling pathway; IDA.
KW Neuropeptide; Amidation.
FT MOD_RES 10 AA; 1244 MW; 3CFE9C29C4540A8 CRC64;
SQ SEQUENCE 10 AA; 1244 MW; 3CFE9C29C4540A8 CRC64;

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Query Match          31.7%; Score 19; DB 1; Length 10;
Best Local Similarity 44.4%; Pred. No. 7.3e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GYKSKFHR 9
Db 1 GYKSKFHR 9

RESULT 6
MY14_EISFO STANDARD; PRT; 14 AA.
AC P46379;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DZ Myosin-like tetradecapeptide (ERP).
OS Eukarya foetida (Common branding worm) (Common dung-worm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbricina; Lumbricidae; Eisenia.
OX NCBI_TaxID=6396;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Gut;
RX MEDLINE=96087879; PubMed=8532604;
RA Ukeda K., Oumi T., Matsushima O., Ikeda T., Fujita T., Minakata H.,
RA Nomoto K.;
RT "A novel gut tetradecapeptide isolated from the earthworm, Eisenia
RT foetida."
RL Peptides 16:995-999 (1995).
CC -1- FUNCTION: Has a stimulative effect on the contraction of gut
CC muscles.
CC -1- SIMILARITY: TO INSECTS ALLATROPIN.
KM Neuropeptide; Amidation.
FT MOD_RES 14
SQ SEQUENCE 14 AA; 1478 MW; CC9AEFF941CD91AD CRC64;

Query Match          31.7%; Score 19; DB 1; Length 14;
Best Local Similarity 30.0%; Pred. No. 1e+03;
Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 GYKSKFHR 10
Db 1 GYKSKFHR 10

RESULT 7
LCK6_LEUMA STANDARD; PRT; 8 AA.
AC P19988;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DZ Leucokinin VI (L-VI).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberidae;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RX MEDLINE=87052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
RT myotropic peptides of Leucophaea maderae."
RL Comp. Biochem. Physiol. 88C:27-30 (1987).
CC -1- FUNCTION: This cephalomyotropic peptide stimulates contractile
CC activity of cockroach proctodeum (hindgut).
CC -1- SUBCELLULAR LOCATION: Secreted.
DR PIR; J03016; J03016.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.

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FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 935 MW; 9D6365B1E9D5A56 CRC64;

Query Match          30.0%; Score 18; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 SKTH 8
Db 2 SSFH 5

RESULT 8
ASL1_BACSE STANDARD; PRT; 11 AA.
AC P81146;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acharan sulfate lyase 1 (EC 4.2.2.-) (Fragment).
OS Bacteroides stercoris.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=46506;
RN [1]
RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.
RC STRAIN=HT-15;
RX MEDLINE=21223019; PubMed=11322884;
RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;
RT "Purification and characterization of acharan sulfate lyases, two
RT novel heparinases, from Bacteroides stercoris HT-15."
RL Eur. J. Biochem. 268:2635-2641 (2001).
CC -1- FUNCTION: Degrades acharan sulfate and, to a lesser extent,
CC heparin and heparan sulfate.
CC -1- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and cobalt.
CC Activated by reducing agents, such as DL-dithiothreitol and 2-
CC mercaptoethanol.
CC -1- SUBUNIT: Monomer.
CC -1- PTM: The N-terminus is blocked.
CC -1- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is
CC 7.2 and optimum temperature 45 degrees Celsius.
CC Lyase; Heparin-binding.
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1395 MW; 01B2DAA241E865AB CRC64;

Query Match          30.0%; Score 18; DB 1; Length 11;
Best Local Similarity 25.0%; Pred. No. 1.3e+03;
Matches 2; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 YKSKFHR 9
Db 4 YKSKFHR 11

RESULT 9
CXLI_CONMR STANDARD; PRT; 11 AA.
AC P58607;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lambda-conotoxin CMV1A.
OS Conus marmoreus (Marble cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbecoconcha; Hygastropoda;
OC Neogastropoda; Conidae; Conidae; Conus.
OX NCBI_TaxID=4752;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=20564325; PubMed=10988292;

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RA Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,
 RA Seow K.T., Bay B.-H.;
 RT "lambda-conotoxins, a new family of conotoxins with unique disulfide
 RT pattern and protein folding. Isolation and characterization from the
 RT venom of *Conus marmoreus*.";
 RL J. Biol. Chem. 275:39516-39522(2000).
 CC -1- FUNCTION: Inhibits the neuronal noradrenaline transporter.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- MASS SPECTROMETRY: MW=1237.93; MW ERR=0.21; METHOD=Electrospray.
 CC -1- SIMILARITY: Belongs to the chi/lambda-conotoxin family.
 KM Neurotoxin; Toxin; Hydroxylation.
 FT DISULFID 2 11
 FT MOD RES 10 10 HYDROXYLATION.
 SQ SEQUENCE 11 AA; 1226 MW; 277AAC60B7232B58 CRC64;
 Query Match 30.0%; Score 18; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYK 3
 DB 4 GYK 6

RESULT 10
 ID CXL4_CONMR STANDARD; PRT; 13 AA.
 AC P58810;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lambda/chi-conotoxin Mr1B (Chi-Mr1B).
 OS *Conus marmoreus* (Marble cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbecoconcha; Hypogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=42752;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND STRUCTURE BY NMR.
 RC TISSUE=Venom;
 RX MEDLINE=21419681; PubMed=11528421;
 RA Sharpe I.A., Gehrmann J., Loughnan M.L., Thomas L., Adams D.A.,
 RA Atkins A., Palant E., Craik D.J., Adams D.J., Alewood P.F.,
 RA Lewis R.J.;
 RT "Two new classes of conopeptides inhibit the alpha1-adrenoceptor and
 RT noradrenaline transporter.";
 RL Nat. Neurosci. 4:902-907(2001).
 CC -1- FUNCTION: Inhibits the neuronal noradrenaline transporter.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- PTM: Exists in two forms, due to cis-trans isomerization at His-
 CC 11-Hyp12.
 CC -1- MASS SPECTROMETRY: MW=1393.52; METHOD=Electrospray.
 CC -1- SIMILARITY: Belongs to the chi/lambda-conotoxin family.
 DR PDB; 1IEO; 03-Apr-02.
 KM Neurotoxin; Toxin; Hydroxylation; 3D-structure.
 FT DISULFID 4 13
 FT MOD RES 12 12 HYDROXYLATION.
 SQ SEQUENCE 13 AA; 1382 MW; 277AAC376EAD2B58 CRC64;
 Query Match 30.0%; Score 18; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYK 3
 DB 6 GYK 8

RESULT 11

FARP CALSI
 ID FARP CALSI STANDARD; PRT; 9 AA.
 AC P38435;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRamide-like neuropeptide.
 OS *Callinectes sapidus* (Blue crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Brachyura; Portunoidae; Portunidae; Callinectes.
 OX NCBI_TaxID=6763;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92270479; PubMed=1815216;
 RA Krajinak K.G.;
 RT "The identification and structure-activity relations of a
 RT cardioactive FMRamide-related peptide from the blue crab *Callinectes*
 RT *sapidus*.";
 RL Peptides 12:1295-1302(1991).
 CC -1- FUNCTION: Cardioactive peptide.
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
 CC family.
 KM Neuropeptide; Amidation.
 FT MOD RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 1159 MW; 134F0729D5A4045B CRC64;
 Query Match 28.3%; Score 17; DB 1; Length 9;
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GYKNS 5
 DB 1 GYKNS 5

RESULT 12
 ID COXM RAT STANDARD; PRT; 10 AA.
 AC P80431;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome c oxidase polypeptide VIIb, mitochondrial (EC 1.9.3.1)
 DE (Fragment).
 GN COX7B.
 OS *Rattus norvegicus* (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RC SPRAIN-Wistar; TISSUE=Liver;
 RX MEDLINE=95324529; PubMed=7601105;
 RA Schaeffer H., Noack H., Halanek W., Brandt U., von Jagow G.;
 RT "Cytochrome c oxidase in developing rat heart. Enzymic properties and
 RT amino-terminal sequences suggest identity of the fetal heart and the
 RT adult liver isoform.";
 RL Eur. J. Biochem. 230:235-241(1995).
 CC -1- FUNCTION: This protein is one of the nuclear-coded polypeptide
 CC chains of cytochrome c oxidase, the terminal oxidase in
 CC mitochondrial electron transport.
 CC -1- CATALYTIC ACTIVITY: 4 ferri-cytochrome c + O(2) = 4 ferri-cytochrome
 CC c + 2 H(2)O.
 DR PIR; S65387; S65387.
 KM Oxidoreductase; Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1210 MW; CFC70EB771A3326 CRC64;
 Query Match 28.3%; Score 17; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 KNSKXH 8
DB 5 KTFPEH 10

RESULT 13

REF_CLOPA
ID REF_CLOPA STANDARD; PRT; 11 AA.
AC P81350;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G (EF-G) (CP 5) (Fragment).
GN FUSA.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
sequence analysis of proteins from Clostridium pasteurianum W5.";
RI Electrophoresis 19:802-806(1998).
CC -1- FUNCTION: This protein promotes the GTP-dependent translocation of
the nascent protein chain from the A-site to the P-site of the
ribosome.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC EF-G/EF-2 subfamily.
DR InterPro; IPR000795; EF_GTPbind.
DR PROSITE; PS00301; EFACITOR_GTP; PARTIAL.
KM Elongation factor; Protein biosynthesis; GTP-binding.
FT NON TER 11 11
SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;

Query Match 28.3%; Score 17; DB 1; Length 11;
Best Local Similarity 33.3%; Pred. No. 1.9e+03;
Matches 3; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 YKSKXPHRV 10
DB 2 YPLEKFPNT 10

RESULT 14
NKSXN_PSETE
ID NKSXN_PSETE STANDARD; PRT; 11 AA.
AC P59072;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Short neurotoxin NI (Alpha neurotoxin) (Fragment).
OS Pseudonaja textilis (Eastern brown snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Acanthophiinae; Pseudonaja.
OX NCBI_TaxID=8673;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=9449602; PubMed=10518793;
RA Gong N.L., Armagam A., Jeyaseelan K.;
RT "Postsynaptic short-chain neurotoxins from Pseudonaja textilis: cDNA
cloning, expression and protein characterization.";
RN Bur J. Biochem. 265:982-989(1999).
CC -1- FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic
acetylcholine receptors (nAChR).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- MASS SPECTROMETRY: MW=6236; METHOD=Electrospray.

CC -1- MISCELLANEOUS: LD(50) is 0.84 mg/kg by intravenous injection.
CC -1- SIMILARITY: Belongs to the snake toxin family.
DR InterPro; IPR003571; Snake toxin.
DR PROSITE; PS00272; SNAKE_TOXIN; PARTIAL.
KM Toxin; Neurotoxin; Postsynaptic neurotoxin;
KW Acetylcholine receptor inhibitor; Multigene family.
FT UNSURE 3 3
FT NON TER 11 11
SQ SEQUENCE 11 AA; 1319 MW; 0D1EFC81B58732B CRC64;

QY 1 GYKNS 5
DB 6 GYRDT 10

RESULT 15

MY14_PHEVI
ID MY14_PHEVI STANDARD; PRT; 14 AA.
AC P46980;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Myoactive tetradecapeptide (PTP).
OS Pheretima vittata (Earthworm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbricina; Megascloecidae; Pheretima.
OX NCBI_TaxID=46674;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Gut;
RX MEDLINE=96087879; PubMed=8532604;
RA Ukena K., Ouml T., Matsushima O., Ikeda T., Fujita T., Minakata H.,
RA Nomoto K.;
RT "A novel gut tetradecapeptide isolated from the earthworm, Eisenia
foetida.";
RI Peptides 16:995-999(1995).
CC -1- FUNCTION: Has a stimulative effect on the contraction of gut
muscles.
CC -1- SIMILARITY: TO INSECTS ALLATOTROPIN.
CC Neuropeptide; Amidation.
FT MOD RES 14 14
SQ SEQUENCE 14 AA; 1522 MW; DA0BBE67CCD91AD CRC64;

Query Match 28.3%; Score 17; DB 1; Length 14;
Best Local Similarity 20.0%; Pred. No. 2.5e+03;
Matches 2; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 GYKSKXPHRV 10
DB 1 GFRDGSADRI 10

RESULT 16
LCK4_LEUMA
ID LCK4_LEUMA STANDARD; PRT; 8 AA.
AC P21173;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Leucokinin IV (L-IV).
OS Leucophaea maderae (Madeira cockroach).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
CC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;

RT "Primary structure and synthesis of two additional neuropeptides from *Leucophaea maderae*: members of a new family of Cephalomyotopins." RT Comp. Biochem. Physiol. 84C:271-276 (1986). CC -1- FUNCTION: This cephalomyotropic peptide stimulates contractile activity of cockroach proctodaeum (hindgut). CC -1- SUBCELLULAR LOCATION: Secreted. CC Neuropeptide; Amidation. FT MOD RES 8 AMIDATION. SQ SEQUENCE 8 AA; 906 MW; DC6365B1E9D5BDDA CRC64;

Query Match 26.7%; Score 16; DB 1; Length 8; Best Local Similarity 40.0%; Pred. No. 1.4e+05; Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSKPH 8
D 1 DASFH 5

RESULT 17

ID FAR2_PENMO STANDARD; PRT; 10 AA.
AC P83317;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLP2 (A5SNLWLR-amide).
OS Pennaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea; OC Penaeidae; Pennaeus.
OK NCBI_Taxid=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eye stalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S., Chaitavithangkur P., Sithigorngul W., Petsom A.; "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk of the giant tiger prawn *Pennaeus monodon*." RT Comp. Biochem. Physiol. 131B:325-337 (2002).
RL -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1260.0; METHOD=MALDI.
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.
DR GO:0007218; P-neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD RES 10 AMIDATION.
SQ SEQUENCE 10 AA; 1260 MW; 88F9023B54472455 CRC64;

Query Match 26.7%; Score 16; DB 1; Length 10; Best Local Similarity 37.5%; Pred. No. 2.7e+03; Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 YNSKPHR 9
D 2 YSNLWLR 9

RESULT 18

ID TKL4_LOCM1 STANDARD; PRT; 10 AA.
AC P30250;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Locustachykinin IV (TK-IV).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Peerygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha; OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OK NCBI_Taxid=7004;

RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=91219696; PubMed=2132575;
RA Schoofs L., Holman G.M., Hayes T.K., Kochansky J.P., Nachman R.J., de Loof A.; "Locustachykinin II and IV: two additional insect neuropeptides with homology to peptides of the vertebrate tachykinin family." RT Regul. Pept. 31:199-212 (1990).
CC -1- FUNCTION: Myoactive peptide. Stimulates the contraction of the oviduct and foregut.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
DR PIR; B60073; ECLQAM.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD RES 10 AMIDATION.
SQ SEQUENCE 10 AA; 1040 MW; 9E52CD71E9C97735 CRC64;

Query Match 26.7%; Score 16; DB 1; Length 10; Best Local Similarity 75.0%; Pred. No. 2.7e+03; Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 FHRV 10
D 6 FHRV 9

RESULT 19

ID ANGT_HORSE STANDARD; PRT; 14 AA.
AC P01016;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Angiotensinogen [contains: Angiotensin I (Ang I); Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)] (Fragment).
DE (Fragment).
GN AGT OR SERPINB8.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OK NCBI_Taxid=9796;
RN [1]
RP SEQUENCE.
RA Skeggs L.T. Jr., Kahn J.R., Lentz K., Shumway N.P.; "The preparation, purification, and amino acid sequence of a polypeptide renin substrate." RT J. Exp. Med. 106:439-453 (1957).
RL -1- FUNCTION: In response to lowered blood pressure, the enzyme renin cleaves angiotensin I, from angiotensinogen. AGC (angiotensin converting enzyme) then removes a dipeptide to yield the physiologically active peptide angiotensin II, the most potent pressor substance known, which helps regulate volume and mineral balance of body fluids.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -1- SIMILARITY: Belongs to the serpin family.
DR PIR; A92775; A01250.
DR PDB; 1ER8; 15-OCT-91.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW vasoconstrictor; plasma; Serpin; 3D-structure.
FT PEPTIDE 1 10 ANGIOTENSIN I.
FT PEPTIDE 1 8 ANGIOTENSIN II.
FT PEPTIDE 2 8 ANGIOTENSIN III.
FT NON TER 14 14
SQ SEQUENCE 14 AA; 1759 MW; 2B9921F8BEEFBD7 CRC64;

Query Match 26.7%; Score 16; DB 1; Length 14; Best Local Similarity 40.0%; Pred. No. 3.9e+03; Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 FHRVI 11

Db 8 FULLV 12

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RESULT 20
RS19_CLOPP STANDARD; PRT; 14 AA.
ID RS19_CLOPP
AC 046238;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S19 (Fragment).
GN RPS19.
OS Clover proliferation phytoplasmata.
OC Bacteria; Firmicutes; Mollicutes; Acholoplasmatales;
OC Acholoplasmataceae; Phytoplasmata.
OX NCBI_TaxID=35776;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94350802; PubMed=8071198;
RA Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmata): a basis for
their classification."
RL U. Bacteriol. 176:5244-5254(1994).
CC -1- FUNCTION: Protein S19 forms a complex with S13 that binds strongly
to the 16S ribosomal RNA (By similarity).
CC -1- SIMILARITY: Belongs to the S19p family of ribosomal proteins.
CC -----
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CC -----
CC EMBL: L27011; AAA83944.1; -.
CC HAMAP: MF_00531; -.
CC DR InterPro: IPR002222; RIBOSOMAL_S19; PARTIAL.
CC DR PROSITE: PS00323; RIBOSOMAL_S19; PARTIAL.
CC KW Ribosomal protein; rRNA-binding.
CC FT NON TER 1 1
SQ SEQUENCE 14 AA; 1642 MW; 20C478EB9FFFE4A8 CRC64;

Query Match
Best Local Similarity 26.7%; Score 16; DB 1; Length 14;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 KNSK 6
Db 10 KNOX 13

RESULT 21
RS19_LOMBP STANDARD; PRT; 14 AA.
ID RS19_LOMBP
AC 046878;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S19 (Fragment).
GN RPS19.
OS Locofah witches'-broom phytoplasmata.
OC Bacteria; Firmicutes; Mollicutes; Acholoplasmatales;
OC Acholoplasmataceae; Phytoplasmata.
OX NCBI_TaxID=35773;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94350802; PubMed=8071198;
RA Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmata): a basis for
their classification."
RL U. Bacteriol. 176:5244-5254(1994).

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CC -1- FUNCTION: Protein S19 forms a complex with S13 that binds strongly
to the 16S ribosomal RNA (By similarity).
CC -1- SIMILARITY: Belongs to the S19p family of ribosomal proteins.
CC -----
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modified and this statement is not removed. Usage by and for commercial
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L27027; AAA83944.1; -.
CC DR HAMAP: MF_00531; -.
CC DR InterPro: IPR002222; RIBOSOMAL_S19; PARTIAL.
CC DR PROSITE: PS00323; RIBOSOMAL_S19; PARTIAL.
CC KW Ribosomal protein; rRNA-binding.
CC FT NON TER 1 1
SQ SEQUENCE 14 AA; 1642 MW; 20C478EB9FFFE4A8 CRC64;

Query Match
Best Local Similarity 26.7%; Score 16; DB 1; Length 14;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 KNSK 6
Db 10 KNOX 13

RESULT 22
RS1_ERWCH STANDARD; PRT; 8 AA.
ID RS1_ERWCH
AC P37585;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE 30S ribosomal protein S1 (Fragment).
GN RPSA.
OS Erwinia chrysanthemi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=556;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=3937;
RA Douville A., Toussaint A., Paelen M.;
RL Submitted (Aug-1993) to the EMBL/GenBank/DBJ databases
CC -1- FUNCTION: BINDS mRNA, THUS FACILITATING RECOGNITION OF THE
INITIATION POINT. IT IS NEEDED TO TRANSLATE mRNA WITH A SHORT
SHINE-DALGARNO (SD) PURINE-RICH SEQUENCE (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to the S1p family of ribosomal proteins.
CC -----
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CC -----
CC EMBL: X74750; CA52769.1; -.
CC DR PIR: S37141; S37141.
CC KW Ribosomal protein; Repeat; RNA-binding.
CC FT NON TER 1 1
SQ SEQUENCE 8 AA; 837 MW; 9E18733DC5B339CD CRC64;

Query Match
Best Local Similarity 25.0%; Score 15; DB 1; Length 8;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKSK 6
Db 2 FKSK 6

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RESULT 23

UTAD_HUMAN STANDARD; PRT; 9 AA.
 ID ULAD_HUMAN P31929;
 AC P31929;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of liver tissue (Spot 106) (Fragment).
 OS Homo sapiens (Human); Chordata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=94147969; PubMed=8313870;
 RA Hughes G.J., Frutiger S., Faguet N., Pasquali C., Sanchez J.-C.,
 RA Tissot J.-D., Baloch A., Appel R.D., Hochstrasser D.F.;
 RT "Human liver protein map: update 1993."
 RL Electrophoresis 14:1216-1222(1993).
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 6, its MW is: 15 kDa.
 DR SWISS-2DPAGE; P31929; HUMAN.
 FT NON_TER
 SQ SEQUENCE 9 AA; 1129 MW; D02DFB41B6D3322 CRC64;

Query Match 25.0%; Score 15; DB 1; Length 9;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;
 Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 KNSKFF 8
 DB 3 KKQTVH 8

RESULT 24
 TKX1_SCYCA STANDARD; PRT; 10 AA.
 ID TKX1_SCYCA P08608;
 AC P08608;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Scyliorhinus I.
 OS Scyliorhinus canicula (spotted dogfish) (Spotted catshark);
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphi; Galeoidea; Carcharhiniformes;
 OC Scyliorhinidae; Scyliorhinus.
 NCBI_TaxID=7830;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=86192829; PubMed=2422058;
 RA Conlon J.M., Deacon C.F., O'Toole L., Thim L.,
 RA "Scyliorhinin I and II: two novel tachykinins from dogfish gut.";
 RT FEBS Lett. 200:111-116(1986).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=93292508; PubMed=7686693;
 RA Waugh D., Wang Y., Hazen N., Balmont R.V., Conlon J.M.;
 RA "Primary structures and biological activities of substance-P-related
 RT peptides from the brain of the dogfish, Scyliorhinus canicula.";
 RL Eur. J. Biochem. 214:469-474(1993).
 CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the tachykinin family.
 DR PIR: A24867; A24867.
 DR InterPro: IPR002040; Tachy_Neurokinin.

DR PROSITE; PS00267; TACHYKININ; 1.
 KM Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 10 10
 SQ SEQUENCE 10 AA; 1219 MW; D0602D6B59C33AA9 CRC64;

Query Match 25.0%; Score 15; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 4.2e+03;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KNSKFF 8
 DB 2 KPDKFF 7

RESULT 25
 CA42_LITCI STANDARD; PRT; 11 AA.
 ID CA42_LITCI P82092;
 AC P82092;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE Caerleon 4.2/4.2/4.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
 OC Pelodytidae; Litoria.
 NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Mabit P.A., Bowie J.H., Tyler M.J.;
 RT "Caerleon-like peptides from the skin glands of the Australian blue
 RT mountains tree frog Litoria citropa. Part 1. Sequence determination
 RT using electrospray mass spectrometry.";
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -1- FUNCTION: Hypotensive neuropeptide (probable).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -1- PTM: Isoform 4.2/4 differs from isoform 4.2 in not being
 CC sulfated.
 CC -1- MASS SPECTROMETRY: MW=1404, METHOD=Electrospray.
 CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro: IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE NEG.
 KM Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 FT MOD_RES 1 1
 FT MOD_RES 4 4
 FT MOD_RES 11 11
 FT MOD_RES 11 11
 SQ SEQUENCE 11 AA; 1344 MW; 10DAB894F5B861BB CRC64;

Query Match 25.0%; Score 15; DB 1; Length 11;
 Best Local Similarity 50.0%; Pred. No. 4.6e+03;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YKSKFF 7
 DB 4 YTGSHF 9

RESULT 26
 TKC2_CALVO STANDARD; PRT; 11 AA.
 ID TKC2_CALVO P41518;
 AC P41518;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Callitachykinin II.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.

OK NCBI_TaxID=27454;
 RN (1)
 RP SEQUENCE, AND SYNTHESIS.
 RA MEDLINE=95075727; PubMed=7984492;
 RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,
 Naeser D.R.;
 RT "Callicechykinin I and II, two novel myotropic peptides isolated from
 the blowfly, Calliphora vomitoria, that have resemblances to
 tachykinins.";
 RL Peptides 15:761-768(1994).
 CC -1- FUNCTION: Myoactive peptide.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD RES 11 11
 SQ SEQUENCE 11 AA; 1103 MW; 15D7E3F9C9CDD444 CRC64;

Query Match 25.0%; Score 15; DB 1; Length 11;
 Best Local Similarity 42.9%; Pred. No. 4.6e+03;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYKSKF 7
 |||
 DB 1 GLGNNAF 7

RESULT 27

NP1_LYMST STANDARD; PRT; 13 AA.
 AC P80178;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DE Lymnaea-DP-amide 1
 OS Lymnaea stagnalis (Great pond snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
 OC Lymnaeidae; Lymnaeidae; Lymnaea.
 OX NCBI_TaxID=6523;
 RN (1)
 RP SEQUENCE.
 RC TISSUE=Ganglion;
 RX MEDLINE=93238777; PubMed=8477756;
 RA Johnson A.H., Rehfeld J.F.;
 RT "Lymnaea stagnalis, a new family of neuropeptides from the pond snail,
 Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
 invertebrates?";
 RL Eur. J. Biochem. 213:875-879(1993).
 CC -1- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CKK) FAMILY.
 DR PIR; S32474; S32471.
 KW Neuropeptide; Amidation.
 FT MOD RES 13 13
 SQ SEQUENCE 13 AA; 1519 MW; 9CA07BA3F5D5B455 CRC64;

Query Match 25.0%; Score 15; DB 1; Length 13;
 Best Local Similarity 75.0%; Pred. No. 5.5e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSKF 7
 |||
 DB 7 NSAF 10

RESULT 28

NP4_LYMST STANDARD; PRT; 13 AA.
 AC P80181;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DE Lymnaea-DP-amide 4.
 OS Lymnaea stagnalis (Great pond snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
 OC Lymnaeidae; Lymnaeidae; Lymnaea.

OK NCBI_TaxID=6523;
 RN (1)
 RP SEQUENCE.
 RC TISSUE=Ganglion;
 RX MEDLINE=93238777; PubMed=8477756;
 RA Johnson A.H., Rehfeld J.F.;
 RT "Lymnaea stagnalis, a new family of neuropeptides from the pond snail,
 Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
 invertebrates?";
 RL Eur. J. Biochem. 213:875-879(1993).
 CC -1- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CKK) FAMILY.
 DR PIR; S32474; S32474.
 KW Neuropeptide; Amidation.
 FT MOD RES 13 13
 SQ SEQUENCE 13 AA; 1503 MW; 9CA07BB56D55455 CRC64;

Query Match 25.0%; Score 15; DB 1; Length 13;
 Best Local Similarity 75.0%; Pred. No. 5.5e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSKF 7
 |||
 DB 7 NSAF 10

RESULT 29

TEML_RANTE STANDARD; PRT; 13 AA.
 AC P57104;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Temporin L
 OS Rana temporaria (European common frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8407;
 RN (1)
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=97175050; PubMed=9022710;
 RA Slimaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
 RA Barria D.;
 RT "Temporins, antimicrobial peptides from the European red frog Rana
 temporaria.";
 RL Eur. J. Biochem. 242:788-792(1996).
 CC -1- FUNCTION: Has antibacterial activity against Gram-negative and
 Gram-positive bacteria.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Skin.
 CC -1- SIMILARITY: Belongs to the brevinin family.
 KW Amphibian defense peptide; Antibiotic; Amidation.
 FT MOD RES 13 13
 SQ SEQUENCE 13 AA; 1641 MW; 9EBDCBFAFF7C325 CRC64;

Query Match 25.0%; Score 15; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SKF 7
 |||
 DB 6 SKF 8

RESULT 30

RS19_PPWPB STANDARD; PRT; 14 AA.
 AC Q52033;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 30S ribosomal protein S19 (Fragment).
 GN RPS8 OR RPS19.

OS Pigeon pea witches'-broom phytoplasma.
 OC Bacteria; Firmicutes; Mollicutes; Achleoplasmatales;
 OC Achleoplasmataceae; Phytoplasma.
 OK NCBI_TaxID=37700;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=94350602; PubMed=8071198;
 RX Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
 RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for
 their classification."
 CC CC
 CC J. Bacteriol. 176:524-525 (1994).
 CC -1- FUNCTION: Protein S19 forms a complex with S13 that binds strongly
 to the 16S ribosomal RNA (by similarity).
 CC -1- SIMILARITY: Belongs to the S19 family of ribosomal proteins.
 CC CC
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 or send an email to license@isb-sib.ch).
 CC CC
 CC EMBL: L27036; AAA83946.1; .
 DR HAMAP; MF_00531; -; 1
 DR InterPro; IPR002222; Ribosomal_S19.
 DR PROSITE; PS00323; RIBOSOMAL_S19, PARTIAL.
 KW Ribosomal protein, rRNA-binding.
 FT NON TER 1
 SQ SEQUENCE 14 AA; 1668 MW; 8FD46FB830DFBBA CRC64;
 QY 3 KNSK 6
 Db 6 KDSK 9
 RESULT 31
 SMSI MYOSC STANDARD; PRT; 14 AA.
 AC P20750;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Somatostatin I.
 OS Myoxocephalus scorpius (Shorthorn sculpin) (Daddy sculpin),
 OS Oncorhynchus kisutch (Coho salmon), and
 OS Anguilla anguilla (European freshwater eel).
 OC Bursaria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorphi; Acanthopterygii; Percomorpha; Scorpaeniformes;
 OC Cottidae; Cottidae; Myoxocephalus.
 OK NCBI_TaxID=8097, 8019, 7936;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=M. scorpius; TISSUE=Pancreas;
 RX MEDLINE=89029486; PubMed=2389597;
 RA Conlon J.M., Davis M.S., Falkner S., Thin L.;
 RT "Structural characterization of peptides derived from
 prosomatostatin I and II isolated from the pancreatic islets of two
 species of teleostean fish: the daddy sculpin and the flounder."
 RL Eur. J. Biochem. 168:647-652 (1987).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=O. kisutch; TISSUE=Pancreas;
 RX MEDLINE=87055212; PubMed=2877919;
 RA Piletskyaya E.M., Pollock H.G., Rouse J.B., Hamilton J.W.,
 RA Kimmel J.R., Andrews P.C., Gorman A.;
 RT "Characterization of coho salmon (Oncorhynchus kisutch) islet
 somatostatins.";

RL Gen. Comp. Endocrinol. 63:252-263 (1986).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=A. anguilla; TISSUE=Pancreas;
 RX MEDLINE=89065329; PubMed=2904391;
 RA Conlon J.M., Deacon C.F., Hazen N., Henderson I.W., Thin L.;
 RT "Somatostatin-related and glucagon-related peptides with unusual
 structural features from the European eel (Anguilla anguilla)."
 RL Gen. Comp. Endocrinol. 72:181-189 (1988).
 CC CC
 CC -1- FUNCTION: Somatostatin inhibits the release of somatotropin.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC CC
 CC -1- SIMILARITY: Belongs to the somatostatin family.
 DR PIR; A60840; A60840.
 DR PIR; B60842; B60842.
 DR PIR; S00172; S00172.
 DR InterPro; IPR004250; Somatostatin.
 DR Pfam; PF03002; Somatostatin; 1.
 KW Hormone; Multigene family.
 FT DISUPID 3
 SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;
 QY 1 GYKN 4
 Db 2 GCKN 5
 RESULT 32
 SMSI ALIMI STANDARD; PRT; 14 AA.
 AC P31835;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Somatostatin-14.
 OS Alligator mississippiensis (American alligator), and
 OS Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
 OK NCBI_TaxID=8495, 34903;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=A. mississippiensis; TISSUE=Stomach;
 RX MEDLINE=93324451; PubMed=8101369;
 RA Wang Y., Conlon J.M.;
 RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain
 and stomach of the alligator."
 RL Peptides 14:573-579 (1993).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=T. scripta;
 RX MEDLINE=90341082; PubMed=1974347;
 RA Conlon J.M., Hicks J.W.;
 RT "Isolation and structural characterization of insulin, glucagon and
 somatostatin from the turtle, Pseudemys scripta."
 RL Peptides 11:461-466 (1990).
 CC CC
 CC -1- FUNCTION: Somatostatin inhibits the release of somatotropin.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC CC
 CC -1- SIMILARITY: Belongs to the somatostatin family.
 DR PIR; C60414; C60414.
 DR InterPro; IPR004250; Somatostatin.
 DR Pfam; PF03002; Somatostatin; 1.
 KW Hormone.
 FT DISUPID 3
 SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;
 QY 3
 Db 3
 Query Match 25.0%; Score 15; DB 1; Length 14;
 Best Local Similarity 75.0%; Pred. No. 6e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


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Qy      1 GYKN 4
      1 1 1
      2 GCKN 5

Db

RESULT 33
FAR4 CALVO      STANDARD;      PRT;      9 AA.
ID FAR4 CALVO
AC P41859;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 01-NOV-1995 (Rel. 32, Last annotation update)
DE Calliophora vomitoria 4.
OS Calliophora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Cecidoidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=9219611; PubMed=1549595;
RA Duvé H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliophamides) from the blowfly
RT Calliophora vomitoria."
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
CC DR PIR: D41978; D41978.
CC KM Neuropeptide; Amidation.
CC FT MOD_RES 9
CC SQ SEQUENCE 9 AA; 1182 MW; 31730699CAB6D457 CRC64;

Query Match      23.3%; Score 14; DB 1; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4 NSKFR 9
      1 1 1
      3 NQDFMR 8

Db

RESULT 34
FIBB_PAPHA      STANDARD;      PRT;      9 AA.
ID FIBB_PAPHA
AC P19343;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen beta chain [contains: Fibrinopeptide B] (Fragment).
GN FgB.
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE.
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RA "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RA and Theropithecus gelada): their amino acid sequences and
RA evolutionary rates and a molecular phylogeny for the baboons.";
RL J. Biochem. 94:1973-1978(1983).
CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,

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CC      and thus exposes the N-terminal polymerization sites responsible
CC      for the formation of the soft clot.
CC PIR: E28854; E28854.
CC DR InterPro; IPR002181; Fibrinogen_C.
CC DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
CC KW Blood coagulation; Plasma.
CC FT PEPTIDE 1
CC FT NON_TER 9
CC SQ SEQUENCE 9 AA; 1057 MW; DDFE71B3C7287B06 CRC64;

Query Match      23.3%; Score 14; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 FH 8
      1 1 1
      6 FH 7

Db

RESULT 35
HUTU_KLEAB      STANDARD;      PRT;      9 AA.
ID HUTU_KLEAB
AC P12381;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Urocanate hydratase (EC 4.2.1.49) (Urocanase) (Imidazolepropionate
DE hydrolase) (Fragment).
GN Hutu.
OS Klebsiella aerogenes.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=28451;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88198018; PubMed=2834335;
RA Nieuwkoop A.J., Baldauf S.A., Hudspeth M.E.S., Bender R.A.;
RT "Bidirectional promoter in the hut(p) region of the histidine
RT utilization (hut) operons from Klebsiella aerogenes.";
RL J. Bacteriol. 170:2240-2246(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90368611; PubMed=2203754;
RA Schwacha A., Bender R.A.;
RT "Nucleotide sequence of the gene encoding the repressor for the
RT histidine utilization genes of Klebsiella aerogenes.";
RL J. Bacteriol. 172:5477-5481(1990).
CC -1- CARBOLYTIC ACTIVITY: 3-(5-oxo-4,5-dihydro-3-H-imidazol-4-
CC yl)propanoate = urocanate + H(2)O.
CC -1- COFACTOR: Binds 1 NAD per subunit (By similarity).
CC -1- PATHWAY: Histidine degradation; second step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the urocanase family.
CC
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CC
CC EMBL: M19665; AAA25078.1; -.
CC DR EMBL: M34604; AAA25076.1; -.
CC DR HAMAP: MF_005777.1.
CC DR InterPro; IPR000193; Urocanase.
CC DR PROSITE; PS01233; UROCANASE; PARTIAL.
CC KW Histidine metabolism; Lyase; NAD.
CC FT NON_TER 9
CC SQ SEQUENCE 9 AA; 1140 MW; 970FC41B5325A6C5 CRC64;

Query Match      23.3%; Score 14; DB 1; Length 9;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;

```

Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 SKFRV 10
1111
4 SKYRL 9

Db

RESULT 36

ANGT_BOVIN STANDARD; PRT; 10 AA.

AC P01017;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Angiotensinogen (Contains: Angiotensin I (Ang I); Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin III) (Fragment)).
GN AGT OR SERPINB8.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
OC NCBI_TaxId=9913;
OX NCBI_TaxId=9913;
RN 11
RP SEQUENCE.
RA Elliott D.F., Peart W.S.;
RT "The amino acid sequence in a hypertensin."
RL Biochem J 65:246-254(1957).
CC -1- FUNCTION: In response to lowered blood pressure, the enzyme renin cleaves angiotensin I, from angiotensinogen. ACE (angiotensin converting enzyme) then removes a dipeptide to yield the physiologically active peptide angiotensin II, the most potent pressor substance known, which helps regulate volume and mineral balance of body fluids.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -1- SIMILARITY: Belongs to the serpin family.
DR PIR; A90345; A90345.
DR PDB; 3ER5; 15-JUL-92.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN, PARTIAL.
KW Vasconstrictor; Plasma; Serpin; 3D-structure.
FT PEPTIDE 1 10 ANGIOTENSIN I.
FT PEPTIDE 1 8 ANGIOTENSIN II.
FT PEPTIDE 2 8 ANGIOTENSIN III.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1282 MW; CEEFEDD761F2D842 CRC64;

Query Match 23.3%; Score 14; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 FR 8
111
8 FR 9

Db

RESULT 37

PVK_LOCM1 STANDARD; PRT; 10 AA.

AC P8382;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Periviscerokinin (Lom-PVK-1).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthoptera; Orthoptera; Caellifera; Acridomorpha; Acrididae; Acrididae; Oedipodinae; Locusta.
OC NCBI_TaxId=7004;
OX NCBI_TaxId=7004;
RN 11
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RT TISSUE=Abdominal perisymphathetic organs;

RX MEDLINE=21896327; PubMed=11897380;
RA Predel R., Gaede G.;
RT "Identification of the abundant neuropeptide from abdominal perisymphathetic organs of locusts."
RL Peptides 23:621-627(2002).
CC -1- FUNCTION: Myotropic peptide; increases the frequency of contraction of the heart and stimulates amplitude and tonus of the foregut.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1104.5; METHOD=MALDI.
DR GO; GO:0005576; C:extracellular; IDA.
DR GO; GO:0005184; F:neuropeptide hormone activity; IDA.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IDA.
KM Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1105 MW; 39811269D6DC728 CRC64;

Query Match 23.3%; Score 14; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 KFRV 10
111
6 QFRV 10

Db

RESULT 38

RL16_ACHLA STANDARD; PRT; 10 AA.

AC P29271;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE 50S ribosomal protein L16 (fragment).
GN RPLP.
OS Acholeplasma laidlawi.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales; Acholeplasmataceae; Acholeplasma.
OC NCBI_TaxId=2148;
OX NCBI_TaxId=2148;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=92210505; PubMed=1556079;
RA Ljm P.O., Seare B.B.;
RT "Evolutionary relationships of a plant-pathogenic mycoplasma-like organism and Acholeplasma laidlawi deduced from two ribosomal protein gene sequences."
RL J. Bacteriol. 174:2606-2611(1992).
CC -1- FUNCTION: This protein binds directly to 23S ribosomal RNA and is located at the site of the peptidyltransferase center (By similarity).
CC -1- SIMILARITY: Belongs to the L16P family of ribosomal proteins.
CC -----
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CC -----
DR EMBL; M74771; AAA21914.1; -
DR PIR; F41839; F41839.
DR InterPro; IPR000114; Ribosomal L16.
DR PROSITE; PS00586; RIBOSOMAL_L16_1; PARTIAL.
DR PROSITE; PS00701; RIBOSOMAL_L16_2; PARTIAL.
KM Ribosomal protein; rRNA-binding.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1324 MW; B3386A21B4032766 CRC64;

Query Match 23.3%; Score 14; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 KNSKF 7
: :
5 KRTKY 9

RESULT 39

TRP8_LEUMA STANDARD; PRT; 10 AA.
ID TRP8_LEUMA
AC P81740;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tachykinin-related peptide 8 (IleuMP 8).
OS Leucophaea maderae (Madelira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberidae;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]

RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Brain;
RX MEDLINE=97269266; PubMed=9114447;
RT Muren J.E., Naessel D.R.;
RT "Seven tachykinin-related peptides isolated from the brain of the
RT madeira cockroach, evidence for tissue-specific expression of
RT isoforms".
RL Peptides 18:7-15(1997).
CC -1- FUNCTION: Myoactive peptide. Increases the amplitude and frequency
CC of spontaneous contractions and tonus of hindgut muscle.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Brain.
CC -1- MASS SPECTROMETRY: MW=1076.9; METHOD=MALDI.
CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KM Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1076 MW; 9E410371E9C87685 CRC64;

Query Match 23.3%; Score 14; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 FH 8
: :
6 FH 7

RESULT 40
TKN_PHYFU STANDARD; PRT; 11 AA.
ID TKN_PHYFU
AC P08615;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Physalaemin.
OS Physalaemus fuscumaculatus (Neotropical frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Leptodactylidae;
OC Leptodactylinae; Physalaemus.
OX NCBI_TaxID=8378;
RN [1]

RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=6076612; PubMed=5857249;
RA Erspamer V., Anastasi A., Bertaccini G., Cei J.M.;
RT "Structure and pharmacological actions of physalaemin, the main
RT active polypeptide of the skin of Physalaemus fuscumaculatus.";
RT Experimentia 20:489-490(1964).
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretegones, and contract (directly or indirectly) many smooth
CC muscles.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.

CC -1- SIMILARITY: Belongs to the tachykinin family.
DR PIR; S07201; S07201.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR Pfam; PF02202; Tachykinin_1.
DR PROSITE; PS00267; TACHYKININ; 1.
KM Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KM Pyroliidone carboxylic acid.
FT MOD_RES 1 1
FT MOD_RES 11 11
SQ SEQUENCE 11 AA; 1283 MW; 3293693E59C33457 CRC64;

Query Match 23.3%; Score 14; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 7.1e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SKFH 8
: :
5 NKFY 8

RESULT 41
LICH_BACLI STANDARD; PRT; 12 AA.
ID LICH_BACLI
AC P82907;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lichenin.
OS Bacillus licheniformis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1402;
RN [1]

RP SEQUENCE.
RC STRAIN=26L-10/3RA;
RX MEDLINE=21460732; PubMed=11576300;
RA Pattenalk P., Kaushik J.K., Grover S., Batish V.K.;
RT "Purification and characterization of a bacteriocin-like compound
RT (lichenin) produced anaerobically by Bacillus licheniformis isolated
RT from water buffalo.";
RL J. Appl. Microbiol. 91:636-645(2001).
RN [2]

RP SEQUENCE.
RC STRAIN=26L-10/3RA;
RA Pattenalk P.;
RT "Biochemical characterization and molecular genetics of bacteriocin
RT produced by a selected rumen bacterial isolate." / Karnal, India.
RL Thesis (1999), National Dairy Research Institute / Karnal, India.
CC -1- FUNCTION: OXYGEN LABILE BACTERIOCIN-LIKE. HAS ANTIBACTERIAL
CC ACTIVITY.
CC -1- SUBCELLULAR LOCATION: Secreted.
KW Antibiotic; Bacteriocin.
SQ SEQUENCE 12 AA; 1414 MW; 1C059B6CED4AEEB0 CRC64;

Query Match 23.3%; Score 14; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 FH 8
: :
9 FH 10

RESULT 42
XYLA_STRVN STANDARD; PRT; 12 AA.
ID XYLA_STRVN
AC P14405;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Xylose isomerase (EC 5.3.1.5) (Fragment).
GN XYLA.

OS Streptomyces violaceoruber.
CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

CC Streptomyces; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1935;
 RN (1)
 RP SEQUENCE.
 RC STRAIN=LMG 7183;
 RX MEDLINE=90104230; PubMed=2604694;
 RA Vangryperre W., Aups C., Kersters-Hilderson H., Tempst P.
 RT "Single active-site histidine in D-xylose isomerase from Streptomyces
 violaceoruber. Identification by chemical derivatization and peptide
 mapping.";
 RT Biochem. J. 263:195-199(1989).
 CC -1- CATALYTIC ACTIVITY: D-xylose = D-xylose.
 CC -1- COFACTOR: Binds 2 magnesium ions per subunit (Potential).
 CC -1- SUBUNIT: Homotetramer.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to the xylose isomerase family.
 DR HAMAP; MF 00455; -; 1.
 DR InterPro: IPR001998; Xylose_isom.
 DR PROSITE; PS00172; XYLOSE_ISOMERASE_1; PARTIAL.
 DR PROSITE; PS00173; XYLOSE_ISOMERASE_2; PARTIAL.
 KW Isomerase; Pentose shunt; Xylose metabolism; Metal-binding; Magnesium.
 FT NON_TER 1 1
 FT ACT_SITE 5 5
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1375 MW; E749268B8B1AAAA1 CRC64;
 Query Match 23.3%; Score 14; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 7.6e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 FH 8
 DB 4 FH 5

RESULT 43
 ID IDHC_PIG STANDARD; PRT; 13 AA.
 AC P20304;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Isocitrate dehydrogenase [NADP] cytoplasmic (EC 1.1.1.42)
 DE (Oxalosuccinate decarboxylase) (IDH) (NADP+-specific IDH) (IDP
 DE (Fragment).
 GN IDH1.
 OS Sus scrofa (Pig).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=87308293; PubMed=2887570;
 RA Bailey J.M., Colman R.F.;
 RT "Isolation of the glutamyl peptide labeled by the nucleotide analogue
 2-(4-bromo-2,3-dioxobutylthio)-1,N(6)-ethenoadenosine
 2',5'-biphosphate in the active site of NADP+-specific isocitrate
 dehydrogenase.";
 RT J. Biol. Chem. 262:12620-12626(1987).
 RN (2)
 RP SEQUENCE.
 RX MEDLINE=87308292; PubMed=3624273;
 RA Ehrlich R.S., Colman R.F.;
 RT "Characterization of an active site peptide modified by the substrate
 analogue 3-bromo-2-ketoglutarate on a single chain of dimeric NADP+-
 dependent isocitrate dehydrogenase.";
 RL J. Biol. Chem. 262:12614-12619(1987).
 CC -1- CATALYTIC ACTIVITY: Isocitrate + NADP(+) = 2-oxoglutarate + CO(2)
 CC + NADPH.
 CC -1- SUBUNIT: Homodimer.
 CC InterPro: IPR001804; Isoch.
 DR PROSITE; PS00470; IDH_IMDH; PARTIAL.
 KW Oxidoreductase; NADP; Tricarboxylic acid cycle.

FT NON_TER 1 1
 FT ACT_SITE 5 5
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1353 MW; 1B640F0B9F7C71E0 CRC64;
 Query Match 23.3%; Score 14; DB 1; Length 13;
 Best Local Similarity 50.0%; Pred. No. 8.5e+03;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYNSK 6
 DB 8 GLSNVK 13

RESULT 44
 ID NEUT_CAVPO STANDARD; PRT; 13 AA.
 AC P32560;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neurotensin (NT).
 GN NTS.
 OS Cavia porcellus (Guinea pig).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN (1)
 RP SEQUENCE.
 RC TISSUE=Small intestine;
 RX MEDLINE=86248085; PubMed=3087775;
 RA Shaw C., Thim L., Conlon J.M.;
 RT "[Ser7]neurotensin: isolation from guinea pig intestine.";
 RL FEBS Lett. 202:187-192(1986).
 CC -1- FUNCTION: Smooth muscle-contracting peptide.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the neurotensin family.
 DR PIR; A53608; A53608.
 KW Vasoactive; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1
 FT MOD_RES 1 1
 SQ SEQUENCE 13 AA; 1680 MW; 4C8314644C4115B3 CRC64;
 Query Match 23.3%; Score 14; DB 1; Length 13;
 Best Local Similarity 66.7%; Pred. No. 8.5e+03;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKN 4
 DB 3 YEN 5

RESULT 45
 ID ADFA_TENMO STANDARD; PRT; 14 AA.
 AC P82965;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Antidiuretic factor A (ADFA) (ADF) (Antidiuretic hormone A) (ADHA).
 OS Tenebrio molitor (Yellow mealworm).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
 CC Tenebrionidae; Tenebrio.
 OX NCBI_TaxID=7067;
 RN (1)
 RP SEQUENCE. FUNCTION. TISSUE SPECIFICITY, AND MASS SPECTROMETRY.
 RC TISSUE=Head;
 RX MEDLINE=21642653; PubMed=11756661;
 RA Engenheer R.A., Nicolson S.W., Schegg K.M., Hull J.J., Schooley D.A.;
 RT "Identification of a potent antidiuretic factor acting on beetle
 Malpighian tubules.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:84-89(2002).
 CC -1- FUNCTION: Strong inhibitor of fluid secretion by the Malpighian

CC tubules. Uses cGMP as a second messenger and inhibits fluid
CC production by decreasing cAMP concentration.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- MASS SPECTROMETRY: MW=1541.58; METHOD=MALDI.
CC -|- SIMILARITY: STRONG, TO THE C-TERMINAL OF T.MOLITOR CUTICULAR
CC PROTEIN LPCP29.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0005184; F:neuropeptide hormone activity; NAS.
DR GO; GO:0007218; P:neuropeptide signaling pathway; NAS.
KW Neuropeptide; Hormone.
SQ SEQUENCE 14 AA; 1543 MW; F49C91A3F16B43D1 CRC64;

Query Match 23.3%; Score 14; DB 1; Length 14;
Best Local Similarity 42.9%; Pred. No. 9.2e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 NSKPRV 10
| : | |
Db 3 NTPGHAV 9

Search completed: August 30, 2004, 10:50:20
Job time : 1.89527 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:41:54 ; Search time 3.30743 Seconds
(without alignments)
319.918 Million cell updates/sec

Title: US-09-720-469A-4

Perfect score: 60

Sequence: 1 GYKSKFHRV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1638

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	41.7	14	2	PT0254
2	23	38.3	13	2	PT0331
3	22	36.7	12	2	PH1454
4	22	36.7	12	2	PC4377
5	22	36.7	13	2	PH0787
6	21	35.0	10	2	B61033
7	20	33.3	9	2	JP0073
8	20	33.3	11	2	PT0211
9	20	33.3	14	2	S22236
10	20	33.3	14	2	S29486
11	19	31.7	13	2	S65381
12	19	31.7	13	2	A61361
13	19	31.7	13	2	S47358
14	18	30.0	8	2	JS0316
15	18	30.0	12	2	PT0274
16	18	30.0	13	2	AS9387
17	17	28.3	9	2	D58503
18	17	28.3	10	2	S65387
19	17	28.3	10	2	PC4374
20	17	28.3	11	2	IS4193
21	17	28.3	11	2	PH0939
22	17	28.3	14	2	S36788
23	16	26.7	9	2	D57444
24	16	26.7	9	2	A42266
25	16	26.7	10	1	ECIO4M
26	16	26.7	10	2	PT0243
27	16	26.7	11	2	S23373
28	16	26.7	12	2	S01222
29	16	26.7	12	2	S10624

30	15	26.7	13	2	A44818	extracellular lipa
31	16	26.7	13	2	S63492	dissimulatory sulf
32	16	26.7	13	2	E60396	antigen 7H8/2 - ma
33	16	26.7	13	2	PS0443	potassium channel
34	16	26.7	14	2	A01250	angiotensin precur
35	16	26.7	14	2	PT0252	Ig heavy chain CRD
36	16	26.7	14	2	PC7079	unidentified 27.2k
37	15	25.0	8	2	S37141	rpsa protein - Erv
38	15	25.0	8	2	B27867	homeotic protein U
39	15	25.0	9	2	PT0324	Ig heavy chain CRD
40	15	25.0	9	2	S78420	ribosomal protein
41	15	25.0	10	2	A24867	scyllorhizin I - s
42	15	25.0	11	2	PC2372	58k heat shock pro
43	15	25.0	11	2	S23926	major glycoprotein
44	15	25.0	12	2	C30503	Ig gamma-2b chain
45	15	25.0	13	2	S32471	lymadPamide 1 - g

ALIGNMENTS

RESULT 1

PT0254
Ig heavy chain CRD3 region (clone 2-115A) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C/Accession: PT0254

R/Yamad, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

U. Exp. Med. 173, 395-407, 1991

A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A/Reference number: PT0222; PMID:9108337; PMID:1699102

A/Accession: PT0254

A/Molecule type: DNA

A/Residues: 1-14 <YAM>

A/Experimental source: B lymphocyte

C/Keywords: heterotetramer; immunoglobulin

Query Match 41.7%; Score 25; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 YKSKFHR 9
DB 7 YDSSGYHR 14

RESULT 2

Ig heavy chain CRD3 region (clone J2-121) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C/Accession: PT0331

R/Yamad, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

U. Exp. Med. 173, 395-407, 1991

A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A/Reference number: PT0222; PMID:9108337; PMID:1699102

A/Accession: PT0331

A/Molecule type: DNA

A/Residues: 1-13 <YAM>

A/Experimental source: B lymphocyte

C/Keywords: heterotetramer; immunoglobulin

Query Match 38.3%; Score 23; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYKSKF 7
DB 6 GYNNPPF 12

RESULT 3

PH1454

T-cell receptor alpha chain (clone A3/72.2) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
 C/Accession: PH1454
 R/Casanova, J.L.; Martinson, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K
 J. Exp. Med. 177, 811-820, 1993
 A/Title: T cell receptor selection by and recognition of two class I major histocompatib
 A/Reference number: PH1430; MUID:93171821; PMID:8436911
 A/Accession: PH1454
 A/Molecule type: mRNA
 A/Residues: 1-12 <CNS>
 A/Experimental source: cytolytic T-lymphocyte
 C/Superfamily: immunoglobulin homology
 C/Keywords: receptor; T-cell

Query Match 36.7%; Score 22; DB 2; Length 12;
 Best Local Similarity 57.1%; Pred. No. 5.7e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYKNSKF 7
 ||:|
 Db 5 GYQNFYF 11

RESULT 4
 PC4377
 telomeric and tetraplex DNA binding protein qTBP42 VIII - rat (fragment)
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 07-May-1999
 C/Accession: PC4377
 R/Sarig, G.; Weisman-Shomer, P.; Fry, M.
 Biochem. Biophys. Res. Commun. 237, 617-623, 1997
 A/Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the CH
 A/Reference number: PC4371; MUID:97445086; PMID:9299414
 A/Accession: PC4377
 A/Molecule type: protein
 A/Residues: 1-12 <SAR>
 C/Comment: This protein binds either strand of the telomeric DNA as well as unimolecular

Query Match 36.7%; Score 22; DB 2; Length 12;
 Best Local Similarity 80.0%; Pred. No. 5.7e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 KFHRY 10
 ||:|
 Db 3 KFHIV 7

RESULT 5
 PH0787
 T-cell receptor alpha chain (F8) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C/Accession: PH0787
 R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
 J. Exp. Med. 174, 1371-1383, 1991
 A/Title: T cell receptor genes in a series of class I major histocompatibility complex-
 allelic exclusion and antigen-specific repertoire.
 A/Reference number: PH0746; MUID:92078846; PMID:1836010
 A/Accession: PH0787
 A/Molecule type: mRNA
 A/Residues: 1-13 <CAS>
 A/Cross-references: EMBL:X60891
 A/Experimental source: T lymphocyte
 C/Keywords: T-cell receptor

Query Match 36.7%; Score 22; DB 2; Length 13;
 Best Local Similarity 57.1%; Pred. No. 6.2e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYKNSKF 7
 ||:|
 Db 6 GYQNFYF 12

RESULT 6
 B61033
 ranatachykinin B - bullfrog
 C/Species: Rana catesbeiana (bullfrog)
 C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000
 C/Accession: B61033; J00427
 R/Kangawa, K.; Kozawa, H.; Hino, J.; Minamino, N.; Matsuo, H.
 Regul. Pept. 42(Suppl. 1), S12, 1992
 A/Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intest
 A/Reference number: A61033
 A/Accession: B61033
 A/Molecule type: protein
 A/Residues: 1-10 <KAN>
 R/Kozawa, H.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H.
 Biochem. Biophys. Res. Commun. 177, 588-595, 1991
 A/Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intest
 A/Reference number: J00426; MUID:91254337; PMID:2043143
 A/Accession: J00427
 A/Molecule type: protein
 A/Residues: 1-10 <K0Z>
 C/Superfamily: unassigned animal peptides
 C/Keywords: amidated carboxyl end; neuropeptide
 F10/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 35.0%; Score 21; DB 2; Length 10;
 Best Local Similarity 42.9%; Pred. No. 7.3e+02;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 YKNSKFH 8
 ||:|
 Db 1 YKNSDFY 7

RESULT 7
 JP0073
 ribosomal protein l32 - Leuconostoc mesenteroides (fragment)
 C/Species: Leuconostoc mesenteroides
 C/Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 28-Oct-1994
 C/Accession: JP0073
 R/Ochi, K.
 submitted to JIPD, February 1994
 A/Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal pro
 A/Reference number: JP0042
 A/Accession: JP0073
 A/Molecule type: protein
 A/Residues: 1-9 <OCH>
 C/Keywords: protein biosynthesis; ribosome

Query Match 33.3%; Score 20; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KNSK 6
 ||:|
 Db 6 KNSK 9

RESULT 8
 PT0211
 T-cell receptor alpha chain V-J region (4-1-G.4) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
 C/Accession: PT0211
 R/Nakano, N.; Kikufani, H.; Nishimoto, H.; Kishimoto, T.
 J. Exp. Med. 173, 1091-1097, 1991
 A/Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restrict
 A/Reference number: PT0209; MUID:91217621; PMID:1902501
 A/Accession: PT0211
 A/Molecule type: mRNA
 A/Residues: 1-11 <NAK>
 C/Keywords: T-cell receptor

Query Match 33.3%; Score 20; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYKN 4
DB 8 GYON 11

RESULT 9
S22236
lipoxigenase (EC 1.13.11.12) 1 - barley (fragment)
C/Species: Hordeum vulgare (barley)
C/Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
C/Accession: S22236
R/Dodder, A.; Kokkelink, I.; van der Veen, S.; Valk, B.E.; Schram, A.W.; Douma, A.C.
Biochim. Biophys. Acta 1120, 97-104, 1992
A/Title: Purification and characterization of two lipoxigenase isoenzymes from germinat
A/Reference number: S21772; MUID:92207997; PMID:1554746
A/Accession: S22236
A/Molecule type: protein
A/Residues: 1-14 <DOD>
A/Experimental source: var. Triumph, seed
C/Function:
A/Description: catalyzes the peroxidation of polyunsaturated fatty acids to their corre
C/Superfamily: lipoxigenase
C/Keywords: monomer; oxidoreductase; seed

Query Match 33.3%; Score 20; DB 2; Length 14;
Best Local Similarity 37.5%; Pred. No. 1.6e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 YKSKFHR 9
DB 7 YPNTSDHK 14

RESULT 10
S29486
GTP-binding protein o-rab3 - electric ray (Discopyge ommata) (fragment)
C/Species: Discopyge ommata
C/Date: 22-Nov-1993 #sequence_revision 27-Feb-1997 #text_change 13-Mar-1997
C/Accession: S29486
R/Volkhardt, W.; Pevsner, J.; Elferink, L.A.; Scheller, R.H.
FEBS Lett. 317, 53-56, 1993
A/Title: Association of three small GTP-binding proteins with cholinergic synaptic vesic
A/Reference number: S29485; MUID:93154521; PMID:8428634
A/Accession: S29486
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-14 <VOL>

Query Match 33.3%; Score 20; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 NSKFRHVI 11
DB 6 NONFNHVI 13

RESULT 11
S65381
cytochrome-c oxidase (EC 1.9.3.1) chain VIIb, hepatic - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C/Accession: S65381
R/Schneegger, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.
Eur. J. Biochem. 230, 235-241, 1995
A/Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term
A/Reference number: S65372; MUID:95324529; PMID:7601105
A/Accession: S65381

A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-8 <SCH>
C/Keywords: oxidoreductase

Query Match 31.7%; Score 19; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 FHR 9
DB 6 FHR 8

RESULT 12
A61361
bradykinin-like peptide - Bombina orientalis
C/Species: Bombina orientalis
C/Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 18-Aug-2000
C/Accession: A61361
R/Yasuhara, T.; Hira, M.; Nakajima, T.; Yanaihara, N.; Yanaihara, C.; Hashimoto, T.; Sak
Chem. Pharm. Bull. 21, 1388-1391, 1973
A/Title: Active peptides on smooth muscle in the skin of Bombina orientalis Boulenger an
A/Reference number: A61361; MUID:73256822; PMID:4732297
A/Accession: A61361
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-13 <YAS>
C/Superfamily: unassigned animal peptides
C/Keywords: skin

Query Match 31.7%; Score 19; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KFH 8
DB 11 KFH 13

RESULT 13
S47358
T-cell antigen receptor VT junction beta chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C/Accession: S47358
R/Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A/Description: Human HLA-A*0201 restricted recognition of influenza A is dominated by T c
A/Reference number: S47355
A/Accession: S47358
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LEH>
A/Cross-references: EMBL:Z35682; NID:G527453; PIDN:CAH84751.1; PID:G527454
C/Keywords: T-cell receptor

Query Match 31.7%; Score 19; DB 2; Length 13;
Best Local Similarity 42.9%; Pred. No. 2.3e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 YKSKFHR 8
DB 6 YRNQPH 12

RESULT 14
J50316
leucokinin VI - Madeira cockroach
C/Species: Leucophaea madeira (Madeira cockroach)
C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C/Accession: J50316
R/Holman, G.M.; Cook, B.J.; Nachman, R.J.

Comp. Biochem. Physiol. C 88, 27-30, 1987
 A>Title: Isolation, primary structure, and synthesis of leucokinin V and VI: myotrophic
 A/Reference number: J50315
 A/Accession: J50315
 A/Molecule type: protein
 A/Residues: 1-8 <HOL>
 C/Comment: Leucokinin, a family of cephalomyotrophic peptides, stimulate contractile act
 C/Keywords: amidated carboxyl end; cephalomyotrophic peptide; pyroglutamic acid
 F.1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental
 F.8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match
 Best Local Similarity 30.0%; Score 18; DB 2; Length 8;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 SKFH 8
 |||
 Db 2 SSFH 5

RESULT 15
 PT0274
 Ig heavy chain CRD3 region (clone 3-109B) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C/Accession: PT0274
 R/Iamada, K.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A/Reference number: PT0222; MUID:91108337; PMID:1899102
 A/Accession: PT0274
 A/Molecule type: DNA
 A/Residues: 1-12 <YAM>
 A/Experimental source: B lymphocyte
 C/Keywords: heterotetramer; immunoglobulin

Query Match
 Best Local Similarity 30.0%; Score 18; DB 2; Length 12;
 Best Local Similarity 60.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYKNS 5
 |||
 Db 2 GYSSS 6

RESULT 16
 AS9387
 VCAH-1 5'UTR binding protein - Rana pipiens (fragment)
 C/Species: Rana pipiens
 C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
 C/Accession: AS9387
 R/BANERJEE, H.
 submitted to the Protein Sequence Database, February 2001
 A/Description: Identification and characterization of a novel VCAH-1 5'UTR.
 A/Reference number: AS9387
 A/Accession: AS9387
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-13 <BAN>
 A/Experimental source: CCL-145
 A/Note: VCAH-1 5' untranslated region binding protein with a probable translation inhibi

Query Match
 Best Local Similarity 30.0%; Score 18; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYK 3
 |||
 Db 8 GYK 10

RESULT 17
 D58503

translation elongation factor EF-Tu - unidentified bacterium (fragment)
 C/Species: unidentified bacterium
 C/Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 28-May-1999
 C/Accession: D58503
 R/Binette, U.P.; Binette, M.B.
 submitted to the Protein Sequence Database, October 1996
 A/Description: The proteins of kidney and gallbladder stones.
 A/Reference number: A58501
 A/Accession: D58503
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-9 <BIN>
 A/Experimental source: human bile and stones
 C/Superfamily: translation elongation factor Tu; translation elongation factor Tu homolog
 C/Keywords: GTP binding

Query Match
 Best Local Similarity 28.3%; Score 17; DB 2; Length 9;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;
 Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 GYKNSKFR 9
 |||
 Db 1 GYRQFYFR 9

RESULT 18
 S65387
 cytochrome-c oxidase (BC 1.9.3.1) chain VII b, cardiac - rat (fragment)
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 16-Jul-1999
 C/Accession: S65387; S65386
 R/Schaegger, H.; Noack, H.; Halanek, W.; Brandt, U.; von Uggow, G.
 Eur. J. Biochem. 230, 235-241, 1995
 A/Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term
 A/Reference number: S65372; MUID:95324529; PMID:7601105
 A/Accession: S65387
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-10 <SCH>
 A/Accession: S65386
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-10 <SC2>
 C/Keywords: cardiac muscle; heart; oxidoreductase

Query Match
 Best Local Similarity 28.3%; Score 17; DB 2; Length 10;
 Best Local Similarity 50.0%; Pred. No. 4.3e+03;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 KNSKFR 8
 |||
 Db 5 KPTTFH 10

RESULT 19
 PC4374
 telomeric and tetraplex DNA binding protein qTBP42 IV - rat (fragment)
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 07-May-1999
 C/Accession: PC4374
 R/Serig, G.; Weisman-Shomer, P.; Fry, M.
 Biochem. Biophys. Res. Commun. 237, 617-623, 1997
 A/Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the Cap
 A/Reference number: PC4371; MUID:97445086; PMID:9299414
 A/Accession: PC4374
 A/Molecule type: protein
 A/Residues: 1-10 <SAR>
 C/Comment: This protein binds either strand of the telomeric DNA as well as unimolecular

Query Match
 Best Local Similarity 28.3%; Score 17; DB 2; Length 10;
 Best Local Similarity 42.9%; Pred. No. 4.3e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 NSKFRHV 10
: ||:
Db 4 DXKEHRL 10

RESULT 20

Rhesus blood group CcEe protein - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000
C:Accession: 154193
R:Cherif-Zahar, B.; Le Van Kim, C.; Rouillac, C.; Raynal, V.; Carttron, J.P.; Collin, Y.
Genomics 19, 68-74, 1994
A:Title: Organization of the gene (RHCE) encoding the human blood group RnCcEe antigens
A:Reference number: 154193; PMID:94245182; PMID:8188244
A:Accession: 154193
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-11 <RES>
A:Cross-references: GB:S70456; NID:9546795; PIDN:AD14061.1; PID:G4261761
A:Gene: GDB:RHCE
A:Cross-references: GDB:229957; OMIM:111700
A:Map position: 1p36.2-1p34

Query Match 28.3%; Score 17; DB 2; Length 11;
Best Local Similarity 37.5%; Pred. No. 4.7e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 4 NSKFRHV 11
: ||:
Db 2 SSKYPRSV 9

RESULT 21

T-cell receptor beta chain V-D-J region (clone 10) - rat (fragment)
PH0939
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0939
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy
A:Reference number: PH0891; PMID:92078857; PMID:1836012
A:Accession: PH0939
A:Molecule type: mRNA
A:Residues: 1-11 <GOL>
A:Experimental source: complete Freund's adjuvant-immunized lymph node
C:Keywords: T-cell receptor

Query Match 28.3%; Score 17; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYKNS 5
: ||:
Db 7 GUKNT 11

RESULT 22

dodecenoyl-CoA Delta-isomerase (EC 5.3.3.8) / enoyl-CoA hydratase (EC 4.2.1.17) / 3-hydr
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 07-Nov-1997 #text_change 24-Jul-1998
C:Accession: S36678
R:Chen, N.; Crane, D.I.
Biochem. J. 283, 605-610, 1992
A:Title: Induction of the major integral membrane protein of mouse liver peroxisomes by
A:Reference number: S21285; PMID:9224695; PMID:1575703
A:Molecule type: protein
A:Residues: 1-14 <CHE>
A:Experimental source: liver

C:Function:
A:Pathway: fatty acid beta-oxidation
C:Keywords: carbon-oxygen lyase; fatty acid beta-oxidation; hydro-lyase; intramolecular

Query Match 28.3%; Score 17; DB 2; Length 14;
Best Local Similarity 42.9%; Pred. No. 6.1e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 GYKNSKF 7
: ||:
Db 2 GFKMGPF 8

RESULT 23

neuropeptide Grb-AST B4 - two-spotted cricket
D57444
C:Species: Gryllus bimaculatus (two-spotted cricket)
C:Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C:Accession: D57444
R:Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995
A:Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cri
A:Reference number: A57444; PMID:95403341; PMID:7673141
A:Accession: D57444
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <LOR>

Query Match 26.7%; Score 16; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 KFH 8
: ||:
Db 4 RFH 6

RESULT 24

peptidylglycine monooxygenase (EC 1.14.17.3), rPAM-5 - rat (fragment)
A42266
N:Alternate names: peptidylglycine alpha-amidating monooxygenase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 26-May-1995
C:Accession: A42266
R:Ripper, B.A.; Green, C.B.; Campbell, T.A.; Soffers, D.A.; Keutmann, H.T.; Mains, R.E.
J. Biol. Chem. 267, 4008-4015, 1992
A:Title: Alternative splicing and endoproteolytic processing generate tissue-specific fo
A:Reference number: A42266; PMID:92156145; PMID:1740449
A:Accession: A42266
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-9 <EIP>
A:Experimental source: pituitary
A:Note: sequence extracted from NCBI backbone (NCBI:82733, NCBI:82750)
C:Keywords: oxidoreductase

Query Match 26.7%; Score 16; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYKNS 5
: ||:
Db 4 GFKDT 8

RESULT 25

ECLQ4M
tachykinin IV - migratory locust
N:Alternate names: locusttachykinin IV
C:Species: Locusta migratoria (migratory locust)
C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 08-Dec-1995
C:Accession: B60073
R:Schoofs, L.; Holman, G.M.; Hayes, T.K.; Kochansky, J.P.; Nachman, R.J.; De Loof, A.

Regul. Pept. 31, 199-212, 1990
 A>Title: Locust tachykinin III and IV: two additional insect neuropeptides with homology
 A:Reference number: A60073; PMID:91219696; PMID:2132575
 A:Accession: B60073
 A:Molecule type: protein
 A:Residues: 1-10 <SCH>
 C:Superfamily: tachykinin
 C:Keywords: amidated carboxyl end; neuropeptide; tachykinin
 F:10/Modified site: amidated carboxyl end (Arg) #status experimental

Query Match 26.7%; Score 16; DB 1; Length 10;
 Best Local Similarity 75.0%; Pred. No. 6.6e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 FHRV 10
 |||
 DB 6 FHGV 9

RESULT 26
 PT0243
 Ig heavy chain CRD3 region (clone 2-103A) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PT0243
 R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991

A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A:Reference number: PT0222; PMID:91108337; PMID:1899102
 A:Accession: PT0243
 A:Molecule type: DNA
 A:Residues: 1-10 <YAM>
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match 26.7%; Score 16; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 6.6e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYXS 5
 |||
 DB 2 GYDS 6

RESULT 27
 S23373
 T-cell receptor alpha chain J region - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
 C:Accession: S23373
 R:Pluschke, G.; Ricken, G.; Taube, H.; Kroninger, S.; Melchers, I.; Peter, H.H.; Eichman
 Eur. J. Immunol. 21, 2749-2754, 1991

A>Title: Biased T cell receptor V(alpha) region repertoire in the synovial fluid of rheu
 A:Reference number: S23364; PMID:92037820; PMID:1657615
 A:Accession: S23373
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-11 <PLU>
 A:Cross-references: EMBL:X58168
 C:Keywords: T-cell receptor

Query Match 26.7%; Score 16; DB 2; Length 11;
 Best Local Similarity 42.9%; Pred. No. 7.3e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 SKFHRVI 11
 |||
 DB 4 SNYDKVI 10

RESULT 28
 S01222
 translation elongation factor EF-Tu - Pseudomonas aeruginosa (fragment)

C:Species: Pseudomonas aeruginosa
 C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 26-Aug-1999
 C:Accession: S01222
 R:Hughes, M.A.; Jones, D.S.
 Nucleic Acids Res. 16, 7193, 1988
 A>Title: A fragment of the Pseudomonas aeruginosa genome contains five tRNA genes, four
 A:Reference number: S01222; PMID:88303352; PMID:3136442
 A:Accession: S01222
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-12 <HUG>
 A:Cross-references: EMBL:X07950; NID:G45426; PIDN:CAA30775.1; PID:G45427
 C:Genetics:
 A:Gene: tuFB
 C:Superfamily: translation elongation factor Tu; translation elongation factor Tu homolog
 C:Keywords: GTP binding; protein biosynthesis

Query Match 26.7%; Score 16; DB 2; Length 12;
 Best Local Similarity 75.0%; Pred. No. 8e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 KFRH 9
 |||
 DB 5 KFER 8

RESULT 29
 S10624
 lipovitellin - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
 C:Accession: S10624
 R:Wallace, R.A.; Hoch, K.D.; Carnevali, O.
 J. Mol. Biol. 213, 407-409, 1990

A>Title: Placement of small lipovitellin subunits within the vitellogenin precursor in Xe
 A:Reference number: S10624; PMID:90278951; PMID:2352275
 A:Accession: S10624
 A:Molecule type: protein
 A:Residues: 1-12 <WAL>

Query Match 26.7%; Score 16; DB 2; Length 12;
 Best Local Similarity 75.0%; Pred. No. 8e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 KFRH 9
 |||
 DB 1 KFOR 4

RESULT 30
 A44818
 extracellular lipase - Pseudomonas aeruginosa (fragment)
 C:Species: Pseudomonas aeruginosa
 C:Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997
 C:Accession: A44818
 R:Gilbert, E.J.; Cornish, A.; Jones, C.W.
 U. Gen. Microbiol. 137, 2223-2229, 1991

A>Title: Purification and properties of extracellular lipase from Pseudomonas aeruginosa
 A:Reference number: A44818; PMID:92085040; PMID:1748875
 A:Accession: A44818
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-13 <GIL>
 A:Experimental source: strain TE3265
 A:Note: sequence extracted from NCBI backbone (NCBI:70395)
 C:Superfamily: Pseudomonas triacylglycerol lipase

Query Match 26.7%; Score 16; DB 2; Length 13;
 Best Local Similarity 30.0%; Pred. No. 8.7e+03;
 Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 YNSKFHRVI 11
 |||

```
Db      3 YTOTKPIVL 12

RESULT 31
S63492
disulfidylase sulfite reductase beta chain, soluble - Desulfovibrio desulfuricans (fragm
C:Species: Desulfovibrio desulfuricans
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S63492
R:Steuber, J.; Arendsen, A.F.; Hagen, W.R.; Kroneck, P.M.H.
Eur. J. Biochem. 233, 873-879, 1995
A:Title: Molecular properties of the dissimilatory sulfite reductase from Desulfovibrio
A:Reference number: S63489; MUID:96085152; PMID:8521853
A:Accession: S63492
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <STB>

Query Match      26.7%; Score 16; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GYKNSK 6
      |||
Db      6 GINPKX 11

RESULT 32
E60396
antigen 7H8/2 - malaria parasite (Plasmodium falciparum) (fragments)
C:Species: Plasmodium falciparum
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jun-2000
C:Accession: E60396
R:Limpaiboon, T.; Taylor, D.W.; Jones, G.; Geysen, H.M.; Saul, A.
Southeast Asian J. Trop. Med. Public Health 21, 388-396, 1990
A:Title: Characterization of a Plasmodium falciparum epitope recognized by a monoclonal
A:Reference number: A60396; MUID:91164876; PMID:1706114
A:Accession: E60396
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-13 <LIM>
A:Cross-references: GB:M31305

Query Match      26.7%; Score 16; DB 2; Length 13;
Best Local Similarity 33.3%; Pred. No. 8.7e+03;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      2 YKNSKPHRY 10
      :|::|
Db      1 FLKSEFMKY 9

RESULT 33
PS0443
potassium channel protein SLO G3 - fruit fly (Drosophila melanogaster) (fragment)
C:Species: Drosophila melanogaster
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Feb-1997
C:Accession: PS0443
R:Adelman, J.P.; Shen, K.Z.; Kavanaugh, M.P.; Warren, R.A.; Wu, Y.N.; Jagrutta, A.; Bond
Neuron 9, 209-216, 1992
A:Title: Calcium-activated potassium channels expressed from cloned complementary DNAs.
A:Reference number: JH0697; MUID:92360298; PMID:1497890
A:Accession: PS0443
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-13 <ADB>
C:Comment: This potassium channel is activated by calcium.
C:Genetics:
A:Gene: FlyBase:slo
A:Cross-references: FlyBase:FBgn0003429
C:Keywords: alternative splicing; ion channel; potassium channel; transmembrane protein

Query Match      26.7%; Score 16; DB 2; Length 13;

Best Local Similarity 42.9%; Pred. No. 8.7e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      5 SKPHRYT 11
      |||
Db      7 SKPDLLV 13

RESULT 34
A01250
angiotensin precursor - horse (fragment)
C:Species: Equus caballus (domestic horse)
C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 15-Sep-2003
C:Accession: A92775; A01250
R:Skeggs Jr., L.T.; Kahn, J.R.; Lentz, K.; Shumway, N.P.
J. Exp. Med. 106, 439-453, 1957
A:Reference number: A92775
A:Accession: A92775
A:Molecule type: protein
A:Residues: 1-14 <SKD>
C:Superfamily: Serpin
C:Keywords: blood pressure control; hormone; vasoconstrictor
F:1-10/Product: angiotensin I #status experimental <AN1>
F:1-8/Product: angiotensin II #status experimental <AN2>

Query Match      26.7%; Score 16; DB 2; Length 14;
Best Local Similarity 40.0%; Pred. No. 9.4e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      7 FHRVI 11
      |||
Db      8 FHLIV 12

RESULT 35
PT0252
Ig heavy chain CRD3 region (clone 2-109D) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0252
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:1693102
A:Accession: PT0252
A:Molecule type: DNA
A:Residues: 1-14 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match      26.7%; Score 16; DB 2; Length 14;
Best Local Similarity 33.3%; Pred. No. 9.4e+03;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      2 YKNSKPHRY 10
      :|::|
Db      6 YDSGGYIV 14

RESULT 36
PC7079
unidentified 27.2K protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: PC7079
R:Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.;
Electrophoresis 21, 1853-1871, 2000
A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of t
A:Reference number: PC7072
A:Accession: PC7079
A:Molecule type: protein
A:Residues: 1-14 <TSU>
A:Experimental source: strain C57BL/6Cr Slc, male; brain, striatum
```

C;Keywords: brain

Query Match 26.7%; Score 16; DB 2; Length 14;
 Best Local Similarity 60.0%; Pred. No. 9.4e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YKNSK 6
 |||
 Db 4 YVKK 8

RESULT 37

S37141

rpsa protein - Erwinia chrysanthemi

C;Species: Erwinia chrysanthemi

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Oct-1995

C;Accession: S37141

R;Donouille, A.; Toussaint, A.; Faellen, M.

submitted to the EMBL Data Library, August 1993

A;Description: Identification of the integration host factor genes of E. chrysanthemi.

A;Reference number: S37139

A;Accession: S37141

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-8 <DOU>

A;Cross-references: EMBL:X74750; NID:G399669; PIDN:CA52769.1; PID:G581108

Query Match 25.0%; Score 15; DB 2; Length 8;
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKNSK 6
 |||
 Db 2 FKSAK 6

RESULT 38

B27867

homeotic protein ultrabithorax - fruit fly (Drosophila melanogaster) (fragment)

C;Species: Drosophila melanogaster

C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 23-Feb-1997

C;Accession: B27867

R;Saari, G.; Bienz, M.

EMBO J. 6, 1775-1779, 1987

A;Title: The structure of the ultrabithorax promoter of Drosophila melanogaster.

A;Reference number: A91072

A;Accession: B27867

A;Molecule type: mRNA

A;Residues: 1-8 <SAA>

C;Genetics:

A;Gene: flyBase:Ubx

A;Cross-references: FlyBase:FBgn0003944

C;Keywords: DNA binding; nucleus; transcription regulation

Query Match 25.0%; Score 15; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 NSKFR 9
 |||
 Db 2 NSYFQ 7

RESULT 39

PT0324

Ig heavy chain CRD3 region (clone J2-106C) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PT0324

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J

A;Reference number: PT0222; WUID:91108337; PMID:1899102

A;Accession: PT0324
 A;Molecule type: DNA
 A;Residues: 1-9 <YAM>
 A;Experimental source: B lymphocyte
 C;Keywords: heterotetramer; immunoglobulin

Query Match 25.0%; Score 15; DB 2; Length 9;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYNS 5
 |||
 Db 3 GYGES 7

RESULT 40

S78420

ribosomal protein R441, mitochondrial [validated] - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000

C;Accession: S78420

R;Goldschmidt-Reisin, S.; Grack, H.R.

submitted to the Protein Sequence Database, February 1998

A;Reference number: S78411

A;Accession: S78420

A;Molecule type: protein

A;Residues: 1-9 <GOL>

A;Note: the protein is designated as mitochondrial ribosomal protein L41

C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 25.0%; Score 15; DB 2; Length 9;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;
 Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 SKFRV 10
 |||
 Db 2 NQXRL 7

RESULT 41

A24867

scyllothrin I - smaller spotted catshark

C;Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)

C;Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 18-Aug-2000

C;Accession: A24867; S33301

R;Conlon, J.M.; Deacon, C.F.; O'Toole, L.; Thim, L.

FEBS Lett. 200, 111-116, 1986

A;Title: Scyllothrin I and II: two novel tachykinins from dogfish gut.

A;Reference number: A91359; WUID:86192829; PMID:2422058

A;Accession: A24867

A;Molecule type: protein

A;Residues: 1-10 <CON>

R;Wagh, D.; Wang, Y.; Hazen, N.; Balment, R.J.; Conlon, J.M.

Eur. J. Biochem. 214, 469-474, 1993

A;Title: Primary structures and biological activities of substance-P-related peptides from

A;Reference number: S33300; WUID:93292508; PMID:7685693

A;Accession: S33301

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <WAG>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; neuropeptide

F10/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 25.0%; Score 15; DB 2; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1e+04;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KNSKF 8
 |||
 Db 2 KPFKF 7

RESULT 42

PC2372
 58k heat shock protein groEL [similarity] - Bacillus cereus (strain ts-4) (fragment)
 C:Species: Bacillus cereus
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 C:Accession: PC2372
 R:Matsumoto, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S.
 Biosci. Biotechnol. Biochem. 59, 231-235, 1995
 A:Title: Identification of DNA-binding proteins changed after induction of sporulation
 A:Reference number: PC2369; MUID:95218265; PMID:7766022
 A:Accession: PC2372
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-11 <MAS>
 C:Keywords: heat shock; molecular chaperone; stress-induced protein

Query Match 25.0%; Score 15; DB 2; Length 11;
 Best Local Similarity 60.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KNSKPF 7
 : |||
 Db 2 KDIF 6

RESULT 43

S23926
 major glycoprotein PAS-6 - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 19-Mar-1997 #sequence_revision 01-Feb-1999 #text_change 01-Feb-1999
 C:Accession: S23926
 R:Kim, D.H.; Kanno, C.; Mizokami, Y.
 Biochim. Biophys. Acta 1122, 203-211, 1992
 A:Title: Purification and characterization of major glycoproteins, PAS-6 and PAS-7, from
 A:Reference number: S23926; MUID:92353107; PMID:1643094
 A:Accession: S23926
 A:Molecule type: protein
 A:Residues: 1-11 <KIM>
 C:Keywords: glycoprotein; milk; blocked amino end

Query Match 25.0%; Score 15; DB 2; Length 11;
 Best Local Similarity 75.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYKN 4
 : |||
 Db 3 GNKN 6

RESULT 44

C30503
 Ig gamma-2b chain C region (F5.5.1) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 16-Aug-1996
 C:Accession: C30503
 R:Gilmore, G.L.; Bard, J.A.; Birshtein, B.K.
 J. Immunol. 141, 1754-1761, 1988
 A:Title: DNA rearrangements affecting both variable and constant regions of Ig H chain
 A:Reference number: A30503; MUID:86315788; PMID:2842402
 A:Accession: C30503
 A:Molecule type: mRNA
 A:Residues: 1-12 <GIL>
 A:Experimental source: myeloma cell line
 C:Keywords: immunoglobulin

Query Match 25.0%; Score 15; DB 2; Length 12;
 Best Local Similarity 42.9%; Pred. No. 1.2e+04;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 KNSKPF 9
 : |||
 Db 1 ENYNGHR 7

RESULT 45

S32471
 LymnaeaFamide 1 - great pond snail
 C:Species: Lymnaea stagnalis (great pond snail)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
 C:Accession: S32471
 R:Johnsen, A.H.; Rehfeld, J.F.
 Eur. J. Biochem. 213, 875-879, 1993
 A:Title: LymnaeaFamides, a new family of neuropeptides from the pond snail, Lymnaea stagn
 A:Reference number: S32471; MUID:93287777; PMID:8477756
 A:Accession: S32471
 A:Molecule type: protein
 A:Residues: 1-13 <JOH>
 A:Cross-references: PIDN:AA26362.1; PID:9299829
 A:Experimental source: ganglia
 C:Keywords: amidated carboxyl end; neuropeptide
 F:13/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 25.0%; Score 15; DB 2; Length 13;
 Best Local Similarity 75.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSKF 7
 : |||
 Db 7 NSAP 10

Search completed: August 30, 2004, 10:58:49
 Job time : 4.30743 secs

Thu Sep 2 07:41:37 2004

us-09-720-469a-4.aug30.1rapb

Page 1

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: August 30, 2004, 10:49:45 ; Search time 13.4527 Seconds
(without alignments)
257.253 Million cell updates/sec

Title: US-09-720-469A-4

Perfect score: 60

Sequence: 1 GYKSKFRRV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 149443

Minimum DB seq length: 8

Maximum DB seq length: 14

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PTC_NEM_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEM_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEM_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/PTC_US_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEM_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09_NEM_PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10_NEM_PUB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	53.3	9	US-10-447-161-84	Sequence 84, App1
2	32	53.3	9	US-10-788-016-1	Sequence 1, App1
3	27	45.0	11	US-10-105-232-266	Sequence 266, App
4	27	45.0	11	US-10-189-437-253	Sequence 253, App
5	26.5	44.2	12	US-09-226-666-1	Sequence 1, App1
6	26.5	44.2	12	US-09-226-666-13	Sequence 13, App1
7	26.5	44.2	12	US-09-226-666-16	Sequence 16, App1
8	26	43.3	8	US-10-462-452-459	Sequence 459, App
9	26	43.3	8	US-10-601-953-588	Sequence 588, App
10	26	43.3	8	US-10-322-266-460	Sequence 460, App
11	26	43.3	9	US-09-780-053-158	Sequence 158, App
12	26	43.3	9	US-10-380-705-12	Sequence 12, App1
13	26	43.3	10	US-09-780-053-180	Sequence 180, App
14	26	43.3	10	US-09-780-053-304	Sequence 304, App
15	26	43.3	10	US-09-780-053-399	Sequence 399, App

16	26	43.3	10	US-09-572-270A-759	Sequence 759, App
17	26	43.3	10	US-10-462-452-413	Sequence 413, App
18	26	43.3	10	US-10-601-953-541	Sequence 541, App
19	26	43.3	10	US-10-322-266-414	Sequence 414, App
20	26	43.3	8	US-10-239-313A-642	Sequence 642, App
21	25	41.7	14	US-10-014-485A-116	Sequence 116, App
22	25	41.7	11	US-10-289-456-91	Sequence 91, App1
23	25	41.7	12	US-09-582-172-186	Sequence 186, App
24	25	41.7	9	US-09-582-172-245	Sequence 245, App
25	25	41.7	13	US-10-174-105A-153	Sequence 153, App
26	25	41.7	14	US-10-289-456-108	Sequence 108, App
27	25	41.7	14	US-10-105-232-267	Sequence 267, App
28	25	41.7	14	US-10-105-232-270	Sequence 270, App
29	25	41.7	14	US-10-189-437-254	Sequence 254, App
30	25	41.7	14	US-10-189-437-257	Sequence 257, App
31	24	40.0	8	US-09-910-552-16	Sequence 16, App1
32	24	40.0	8	US-10-643-465-16	Sequence 16, App1
33	24	40.0	15	US-10-117-937-555	Sequence 555, App
34	24	40.0	10	US-09-780-053-472	Sequence 472, App
35	24	40.0	9	US-09-553-126-126	Sequence 126, App
36	24	40.0	10	US-09-896-896A-80	Sequence 80, App1
37	24	40.0	10	US-10-319-340-8	Sequence 8, App1
38	24	40.0	10	US-10-117-937-556	Sequence 556, App
39	24	40.0	10	US-10-330-697-126	Sequence 126, App
40	24	40.0	11	US-09-791-393-21	Sequence 21, App1
41	24	40.0	11	US-09-791-393-21	Sequence 21, App1
42	24	40.0	11	US-10-264-309-22	Sequence 22, App1
43	24	40.0	12	US-10-302-100B-12	Sequence 12, App1
44	24	40.0	14	US-09-734-002-5	Sequence 5, App1
45	24	40.0	14	US-09-932-613-39	Sequence 39, App1

ALIGNMENTS

RESULT 1

US-10-447-161-84

Sequence 84, Application US/10447161

Publication No. US20040023314A1

GENERAL INFORMATION:

APPLICANT: Wang, Rong-fu

TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis

FILE REFERENCE: HO-P02484US1

CURRENT APPLICATION NUMBER: US/10/447,161

CURRENT FILING DATE: 2003-05-28

PRIOR APPLICATION NUMBER: 60/383,530

PRIOR FILING DATE: 2002-05-28

NUMBER OF SEQ ID NOS: 148

SOFTWARE: PatentIn version 3.1

SEQ ID NO 84

LENGTH: 9

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic Peptide

US-10-447-161-84

Query Match

Best Local Similarity 53.3%; Score 32; DB 16; Length 9;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KFRV 11

Db 1 KFRV 6

RESULT 2

US-10-788-016-1

Sequence 1, Application US/10788016

Publication No. US2004014192A1

GENERAL INFORMATION:

APPLICANT: ITOH, Kyogo

TITLE OF INVENTION: Desensitizers

```
/ FILE REFERENCE: 3190-049
/ CURRENT APPLICATION NUMBER: US/10/788,016
/ CURRENT FILING DATE: 2004-02-26
/ PRIOR APPLICATION NUMBER: PCT/JP02/08641
/ PRIOR FILING DATE: 2002-08-28
/ PRIOR APPLICATION NUMBER: JP P2001-260046
/ PRIOR FILING DATE: 2001-08-29
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 1
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Peptide consisting of 9 amino acid residues from the 84th residue
US-10-788-016-1
```

```
Query Match          53.3%: Score 32; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      6 KFHRYI 11
      |||||
Db       1 KFHRYI 6
```

```
RESULT 3
US-10-105-232-266
/ Sequence 266, Application US/10105232
/ Publication No. US20030180328A1
/ GENERAL INFORMATION:
/ APPLICANT: BOGOCCH, SAMUEL
/ TITLE OF INVENTION: REPLICIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
/ FILE REFERENCE: 09425-46904
/ CURRENT APPLICATION NUMBER: US/10/105,232
/ CURRENT FILING DATE: 2002-03-26
/ PRIOR APPLICATION NUMBER: 60/303,396
/ PRIOR FILING DATE: 2001-07-09
/ PRIOR APPLICATION NUMBER: 60/278,761
/ PRIOR FILING DATE: 2001-03-27
/ PRIOR APPLICATION NUMBER: 09/146,755
/ PRIOR FILING DATE: 1998-09-04
/ PRIOR APPLICATION NUMBER: 09/817,144
/ PRIOR FILING DATE: 2001-03-27
/ PRIOR APPLICATION NUMBER: 08/198,139
/ PRIOR FILING DATE: 1994-02-17
/ NUMBER OF SEQ ID NOS: 535
/ SOFTWARE: PatentIn 2.1
/ SEQ ID NO 266
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Influenza virus
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (8)
/ OTHER INFORMATION: gly or gln
US-10-105-232-266
```

```
Query Match          45.0%: Score 27; DB 14; Length 11;
Best Local Similarity 57.1%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      4 NSKFHRY 10
      |||||
Db       3 NEKFHRY 9
```

```
RESULT 4
US-10-189-437-253
/ Sequence 253, Application US/10189437
```

```
/ Publication No. US2003019441A1
/ GENERAL INFORMATION:
/ APPLICANT: BOGOCCH, SAMUEL
/ TITLE OF INVENTION: REPLICIN PEPTIDES AND ANTIBODIES THEREFORE
/ FILE REFERENCE: 09425/46905
/ CURRENT APPLICATION NUMBER: US/10/189,437
/ CURRENT FILING DATE: 2002-07-08
/ PRIOR APPLICATION NUMBER: 10/105,232
/ PRIOR FILING DATE: 2002-03-26
/ PRIOR APPLICATION NUMBER: 09/984,057
/ PRIOR FILING DATE: 2001-10-26
/ PRIOR APPLICATION NUMBER: 60/303,396
/ PRIOR FILING DATE: 2001-07-09
/ PRIOR APPLICATION NUMBER: 60/278,761
/ PRIOR FILING DATE: 2001-03-27
/ NUMBER OF SEQ ID NOS: 729
/ SOFTWARE: PatentIn 2.1
/ SEQ ID NO 253
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Influenza virus
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (8)
/ OTHER INFORMATION: gly or gln
US-10-189-437-253
```

```
Query Match          45.0%: Score 27; DB 14; Length 11;
Best Local Similarity 57.1%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      4 NSKFHRY 10
      |||||
Db       3 NEKFHRY 9
```

```
RESULT 5
US-09-226-666-1
/ Sequence 1, Application US/0922666A
/ Patent No. US20020077282A1
/ GENERAL INFORMATION:
/ APPLICANT: Spaccapoli, Peter
/ APPLICANT: Rothstein, David M.
/ TITLE OF INVENTION: METHOD FOR TREATING CYSTIC FIBROSIS
/ FILE REFERENCE: 50032/007001
/ CURRENT APPLICATION NUMBER: US/09/226,666A
/ CURRENT FILING DATE: 1999-01-08
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Internal fragment
US-09-226-666-1
```

```
Query Match          44.2%: Score 26.5; DB 9; Length 12;
Best Local Similarity 75.0%; Pred. No. 4.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
```

```
QY      1 GYNSKFH 8
      |||||
Db       6 GYNSKFH 12
```

```
RESULT 6
US-09-226-666-13
/ Sequence 13, Application US/0922666A
/ Patent No. US20020077282A1
/ GENERAL INFORMATION:
```

APPLICANT: Spacciapoli, Peter
APPLICANT: Rothstein, David M.
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: METHOD FOR TREATING CYSTIC FIBROSIS
FILE REFERENCE: 50032/007001
CURRENT APPLICATION NUMBER: US/09/226,666A
CURRENT FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Derived from Homo sapiens
US-09-226-666-13

Query Match 44.2%; Score 26.5; DB 9; Length 12;
Best Local Similarity 75.0%; Pred. No. 4.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKSKFH 8
|||
Db 6 GYK-QKFF 12

RESULT 7
US-09-226-666-16
Sequence 16, Application US/09226666A
Patent No. US20020077282A1
GENERAL INFORMATION:
APPLICANT: Spacciapoli, Peter
APPLICANT: Rothstein, David M.
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: METHOD FOR TREATING CYSTIC FIBROSIS
FILE REFERENCE: 50032/007001
CURRENT APPLICATION NUMBER: US/09/226,666A
CURRENT FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Derived from Homo sapiens
US-09-226-666-16

Query Match 44.2%; Score 26.5; DB 9; Length 12;
Best Local Similarity 75.0%; Pred. No. 4.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKSKFH 8
|||
Db 6 GYK-QKFF 12

RESULT 8
US-10-462-452-459
Sequence 459, Application US/10462452
Publication No. US20040037809A1
GENERAL INFORMATION:
APPLICANT: Quay, Steven
APPLICANT: El Shafy, Mohammed Abd
APPLICANT: Gupta, Malini
APPLICANT: de Meireles, Jorge
TITLE OF INVENTION: Compositions and Methods for Enhanced
TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta
FILE REFERENCE: 02-02US
CURRENT APPLICATION NUMBER: US/10/462,452
CURRENT FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/393,066
PRIOR FILING DATE: 2002-06-28

NUMBER OF SEQ ID NOS: 790
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 459
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US-10-462-452-459

Query Match 43.3%; Score 26; DB 12; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KNSKFF 8
|||
Db 1 RNSKFF 6

RESULT 9
US-10-601-953-588
Sequence 588, Application US/10601953
Publication No. US20040077540A1
GENERAL INFORMATION:
APPLICANT: Quay, Steven C.
TITLE OF INVENTION: Compositions And Methods For Modulating Physiology Of Epithelial
TITLE OF INVENTION: Junctional Adhesion Molecules For Enhanced Mucosal Delivery Of
TITLE OF INVENTION: Therapeutic Compounds
FILE REFERENCE: 02-03US
CURRENT APPLICATION NUMBER: US/10/601,953
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: 60/392,512
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 900
SOFTWARE: Patentin Version 3.2
SEQ ID NO 588
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic construct
US-10-601-953-588

Query Match 43.3%; Score 26; DB 16; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KNSKFF 8
|||
Db 1 RNSKFF 6

RESULT 10
US-10-322-266-460
Sequence 460, Application US/10322266
Publication No. US20040115135A1
GENERAL INFORMATION:
APPLICANT: Quay, Steven C.
TITLE OF INVENTION: Compositions And Methods For Enhanced Mucosal Delivery Of Peptide
TITLE OF INVENTION: YY And Methods For Treating And Preventing Obesity
FILE REFERENCE: NP010567
CURRENT APPLICATION NUMBER: US/10/322,266
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 797
SOFTWARE: Patentin Version 3.2
SEQ ID NO 460
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic construct
US-10-322-266-460

Query Match 43.3%; Score 26; DB 16; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KNSKSF 8
: ||| :
Db 1 KNSSF 6

RESULT 11
US-09-780-053-158
; Sequence 158, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Chailita-Bid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-158

Query Match 43.3%; Score 26; DB 9; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYNSKSF 8
|::|||:
Db 1 GHONSTFY 8

RESULT 12
US-10-380-705-12
; Sequence 12, Application US/10380705
; Publication No. US20040019919A1
; GENERAL INFORMATION:
; APPLICANT: Universit, t Zurich
; TITLE OF INVENTION: Calcium binding proteins
; FILE REFERENCE: Calsyntens
; CURRENT APPLICATION NUMBER: US/10/380,705
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: EP 00810830.0
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-380-705-12

Query Match 43.3%; Score 26; DB 15; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKNSKSF 8
|::|||:
Db 2 YKPAPSF 8

RESULT 13

US-09-780-053-180
; Sequence 180, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Chailita-Bid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 180
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-180

Query Match 43.3%; Score 26; DB 9; Length 10;
Best Local Similarity 50.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYNSKSF 8
|::|||:
Db 2 GHONSTFY 9

RESULT 14
US-09-780-053-304
; Sequence 304, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Chailita-Bid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 304
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-304

Query Match 43.3%; Score 26; DB 9; Length 10;
Best Local Similarity 50.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYNSKSF 8
|::|||:
Db 1 GHONSTFY 8

RESULT 15
US-09-780-053-399

```
Sequence 399, Application US/09780053
Patent No. US20020102640A1
GENERAL INFORMATION:
APPLICANT: Rene S. Hubert
APPLICANT: Daniel E.H. Afar
APPLICANT: Pia M. Chailita-Eid
APPLICANT: Mary Farris
APPLICANT: Elana Levin
APPLICANT: Steve Chappell Mitchell
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
FILE REFERENCE: 129,USU1
CURRENT APPLICATION NUMBER: US/09/780,053
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/181,261
PRIOR FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 716
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 399
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-780-053-399

Query Match
Best Local Similarity 43.3%; Score 26; DB 9; Length 10;
Best Local Similarity 50.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYKNSKFH 8
DB 1 GHQNSTFY 8

RESULT 16
US-09-572-270A-759
Sequence 759, Application US/09572270A
Publication No. US20030148368A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd.
TITLE OF INVENTION: Inter- complementary peptide listing
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/572,270A
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 1144
SOFTWARE: ProPatent version 1.0
SEQ ID NO 759
LENGTH: 10
TYPE: PRT
ORGANISM: Arabidopsis Thaliana
OTHER INFORMATION: Sequence located in GL2. at 99-108 and may interact with
US-09-572-270A-759

Query Match
Best Local Similarity 43.3%; Score 26; DB 10; Length 10;
Best Local Similarity 57.1%; Pred. No. 4.9e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KNSKFSRH 9
DB 1 KRKKYHR 7

RESULT 17
US-10-462-452-413
Sequence 413, Application US/10462452
Publication No. US20040037809A1
GENERAL INFORMATION:
APPLICANT: Quay, Steven
APPLICANT: El Shafy, Mohammed Abd
APPLICANT: Gupta, Malini
APPLICANT: de Meireles, Jorge
TITLE OF INVENTION: Compositions and Methods for Enhanced
TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta
```

```
FILE REFERENCE: 02-02US
CURRENT APPLICATION NUMBER: US/10/462,452
CURRENT FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/393,066
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 790
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 413
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-10-462-452-413

Query Match
Best Local Similarity 43.3%; Score 26; DB 12; Length 10;
Best Local Similarity 66.7%; Pred. No. 4.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KNSKFSRH 8
DB 1 RNSSFH 6

RESULT 18
US-10-601-953-541
Sequence 541, Application US/10601953
Publication No. US20040077540A1
GENERAL INFORMATION:
APPLICANT: Quay, Steven C.
TITLE OF INVENTION: Compositions And Methods For Modulating Physiology Of Epithelial
TITLE OF INVENTION: Junctional Adhesion Molecules For Enhanced Mucosal Delivery Of
FILE REFERENCE: 02-03US
CURRENT APPLICATION NUMBER: US/10/601,953
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: 60/392,512
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 900
SOFTWARE: PatentIn version 3.2
SEQ ID NO 541
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic construct
US-10-601-953-541

Query Match
Best Local Similarity 43.3%; Score 26; DB 16; Length 10;
Best Local Similarity 66.7%; Pred. No. 4.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KNSKFSRH 8
DB 1 RNSSFH 6

RESULT 19
US-10-322-266-414
Sequence 414, Application US/10322266
Publication No. US20040115135A1
GENERAL INFORMATION:
APPLICANT: Quay, Steven C.
TITLE OF INVENTION: Compositions And Methods For Enhanced Mucosal Delivery Of Peptide
TITLE OF INVENTION: XY And Methods For Treating And Preventing Obesity
FILE REFERENCE: NRC10567
CURRENT APPLICATION NUMBER: US/10/322,266
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 797
SOFTWARE: PatentIn version 3.2
SEQ ID NO 414
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
```

OTHER INFORMATION: Synthetic construct
US-10-322-266-414

Query Match 43.3%; Score 26; DB 16; Length 10;
Best Local Similarity 66.7%; Pred. No. 4.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KNSKF 8
Db 1 RNSSFH 6

RESULT 20
US-10-239-313A-642
Sequence 642, Application US/10239313A
Publication No. US20030175285A1

GENERAL INFORMATION:
APPLICANT: KLINGNER - HAMOUR, Christine
APPLICANT: CORVAIA, Nathalie
APPLICANT: BECK, Alain
APPLICANT: GOETSCH, Liliane
TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
FILE REFERENCE: 343 727 - US
CURRENT APPLICATION NUMBER: US/10/239.313A
CURRENT FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: FR 00/03711
PRIOR FILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: PCT 01/70772
PRIOR FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 697
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 642
LENGTH: 14
TYPE: PRT
ORGANISM: Clostridium tetani
US-10-239-313A-642

Query Match 43.3%; Score 26; DB 14; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KNSKF 7
Db 5 KNSKF 9

RESULT 21
US-10-014-485A-116
Sequence 116, Application US/10014485A
Publication No. US20020168684A1

GENERAL INFORMATION:
APPLICANT: Cell Signaling Technology, Inc.
APPLICANT: COMB, Michael J.
APPLICANT: ZHANG, Hui
APPLICANT: TAN, Yi
TITLE OF INVENTION: PRODUCTION OF MOTIF-SPECIFIC AND CONTEXT-INDEPENDENT ANTIBODIES
TITLE OF INVENTION: PEPTIDE LIBRARIES AS ANTIGENS
FILE REFERENCE: C81-136 C1P2
CURRENT APPLICATION NUMBER: US/10/014.485A
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: US 09/148,712
PRIOR FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: US 09/535,364
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 145
SOFTWARE: PatentIn version 3.1
SEQ ID NO 116
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:

NAME/KEY: MOD RES
LOCATION: (5)-(5)
OTHER INFORMATION: PHOSPHORYLATION; serine at position 5 is phosphorylated
US-10-014-485A-116

Query Match 41.7%; Score 25; DB 13; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYNSKFH 8
Db 1 GYNSIRH 8

RESULT 22
US-10-289-456-91
Sequence 91, Application US/10289456
Publication No. US20040033211A1

GENERAL INFORMATION:
APPLICANT: Bachmann, Martin
APPLICANT: Mauser, Patrick
APPLICANT: Specht, Gunther
TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
FILE REFERENCE: 1700.0330001
CURRENT APPLICATION NUMBER: US/10/289.456
CURRENT FILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: PCT/IB02/00166
PRIOR FILING DATE: 2002-01-21
PRIOR APPLICATION NUMBER: US 10/050,902
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/396,635
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PatentIn version 3.2
SEQ ID NO 91
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: RANKL peptide EF loop
US-10-289-456-91

Query Match 41.7%; Score 25; DB 12; Length 11;
Best Local Similarity 80.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NSKFH 8
Db 6 NSEFH 10

RESULT 23
US-09-982-172-186
Sequence 186, Application US/09982172
Patent No. US20020137119A1

GENERAL INFORMATION:
APPLICANT: Eml Israel Katz
TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATI
FILE REFERENCE: 01/22283
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: PatentIn version 3.1
SEQ ID NO 186
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Computer generated synthetic peptide

US-09-982-172-186

Query Match 41.7%; Score 25; DB 9; Length 12;
Best Local Similarity 50.0%; Pred. No. 8.9e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 YNKSFKR 9

Db 5 YNSSFYK 12

RESULT 24

US-09-982-172-245
; Sequence 245, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIE
; TITLE OF INVENTION: DIRECTED THERAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAT
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 245
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-245

Query Match 41.7%; Score 25; DB 9; Length 12;
Best Local Similarity 50.0%; Pred. No. 8.9e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 YNKSFKR 9

Db 5 YNSSFYK 12

RESULT 25

US-10-174-105A-153
; Sequence 153, Application US/10174105A
; Publication No. US2003006852A1
; GENERAL INFORMATION:
; APPLICANT: Cell Signaling Technology, Inc.
; APPLICANT: ZHANG, Hui
; APPLICANT: COMB, Michael J.
; APPLICANT: TAN, Yi
; TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIFIC
; TITLE OF INVENTION: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCHING
; FILE REFERENCE: CST-138 CIP3
; CURRENT APPLICATION NUMBER: US/10/174,105A
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 09/148,712
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 09/335,364
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 153
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; NAME/KEY: MOD_RES
; LOCATION: (8)-(8)
; OTHER INFORMATION: PHOSPHORYLATION; serine at position 8 is phosphorylated
US-10-174-105A-153

Query Match 41.7%; Score 25; DB 14; Length 13;
Best Local Similarity 62.5%; Pred. No. 9.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYKSKFH 8

Db 4 GWKNSIRH 11

RESULT 26

US-10-289-456-108
; Sequence 108, Application US/10289456
; Publication No. US2004003321A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Spohn, Gunther
; TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
; FILE REFERENCE: 1700.0330001
; CURRENT APPLICATION NUMBER: US/10/289,456
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/336,635
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 108
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: RANKL peptide EF loop
US-10-289-456-108

Query Match 41.7%; Score 25; DB 12; Length 14;
Best Local Similarity 80.0%; Pred. No. 1e+03; 0; Indels 0; Gaps 0;

QY 4 NSKFK 8

Db 9 NSKFK 13

RESULT 27

US-10-105-232-267
; Sequence 267, Application US/10105232
; Publication No. US20030180328A1
; GENERAL INFORMATION:
; APPLICANT: BOGACH, SAMUEL
; APPLICANT: BOGACH, ELEONORE S.
; TITLE OF INVENTION: REPLICIN PEPTIDES IN RAPID REPLICATION OF GLIOVA CELLS
; TITLE OF INVENTION: AND IN INFLUENZA EPIDEMICS
; FILE REFERENCE: 09425-46904
; CURRENT APPLICATION NUMBER: US/10/105,232
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: PatentIn 2.1

```
; SEQ ID NO 267
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Influenza virus
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)
; OTHER INFORMATION: val or leu
US-10-105-232-267
```

```
Query Match          41.7%; Score 25; DB 14; Length 14;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 4 NSKFF 8
    |||
DB 10 NEKFF 14
```

```
RESULT 28
US-10-105-232-270
; Sequence 270, Application US/10105232
; Publication No. US20030180328a1
; GENERAL INFORMATION:
; APPLICANT: BOGGOCH, SAMUEL
; TITLE OF INVENTION: REPLICIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
; FILE REFERENCE: 09425-46904
; CURRENT APPLICATION NUMBER: US/10/105,232
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 270
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Influenza virus
US-10-105-232-270
```

```
Query Match          41.7%; Score 25; DB 14; Length 14;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 4 NSKFF 8
    |||
DB 10 NEKFF 14
```

```
RESULT 29
US-10-189-437-254
; Sequence 254, Application US/10189437
; Publication No. US20030194414a1
; GENERAL INFORMATION:
; APPLICANT: BOGGOCH, SAMUEL
; TITLE OF INVENTION: REPLICIN PEPTIDES AND ANTIBODIES THEREFORE
; FILE REFERENCE: 09425/46905
; CURRENT APPLICATION NUMBER: US/10/189,437
; PRIOR FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 10/105,232
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/984,057
; PRIOR FILING DATE: 2001-10-26
```

```
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 729
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 254
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Influenza virus
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)
; OTHER INFORMATION: val or leu
US-10-189-437-254
```

```
Query Match          41.7%; Score 25; DB 14; Length 14;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 4 NSKFF 8
    |||
DB 10 NEKFF 14
```

```
RESULT 30
US-10-189-437-257
; Sequence 257, Application US/10189437
; Publication No. US20030194414a1
; GENERAL INFORMATION:
; APPLICANT: BOGGOCH, SAMUEL
; TITLE OF INVENTION: REPLICIN PEPTIDES AND ANTIBODIES THEREFORE
; FILE REFERENCE: 09425/46905
; CURRENT APPLICATION NUMBER: US/10/189,437
; PRIOR FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 10/105,232
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/984,057
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 729
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 257
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Influenza virus
US-10-189-437-257
```

```
Query Match          41.7%; Score 25; DB 14; Length 14;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 4 NSKFF 8
    |||
DB 10 NEKFF 14
```

```
RESULT 31
US-09-910-552-16
; Sequence 16, Application US/09910552
; Publication No. US20020197260A1
; GENERAL INFORMATION:
; APPLICANT: Granooff, Dan M.
; TITLE OF INVENTION: USE OF MONOCLONAL ANTIBODIES THAT DEFINE UNIQUE
; TITLE OF INVENTION: MENINGOCOCCAL B EPITOPES IN THE PREPARATION OF VACCINE
; FILE REFERENCE: 1238.002
; CURRENT APPLICATION NUMBER: US/09/910,552
```



```

:
: CURRENT FILING DATE: 2001-07-23
: PRIOR APPLICATION NUMBER: 09/494,822
: PRIOR FILING DATE: 2000-01-31
: NUMBER OF SEQ ID NOS: 68
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 16
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: sequence from
: OTHER INFORMATION: a phage display peptide library
US-09-910-552-16

```

```
Query Match      40.0%; Score 24; DB 9; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

QY	1	GYKNSKEH	8
Db	1	GYEVQPEH	8

```

RESULT 32
US-10-643-465-16
: Sequence 16, Application US/10643465
: Publication No. US20040077840A1
: GENERAL INFORMATION:
: APPLICANT: Granoff, Dan M.
: APPLICANT: Koe, Gregory R.
: TITLE OF INVENTION: USE OF MONOCLONAL ANTIBODIES THAT DEFINE UNIQUE
: TITLE OF INVENTION: MENINGOCOCCAL B EPITOPES IN THE PREPARATION OF VACCINE
: TITLE OF INVENTION: COMPOSITIONS
: FILE REFERENCE: 1238.002
: CURRENT APPLICATION NUMBER: US/10/643,465
: CURRENT FILING DATE: 2003-08-19
: PRIOR APPLICATION NUMBER: US/08/925,002
: PRIOR FILING DATE: 1997-08-27
: NUMBER OF SEQ ID NOS: 66
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 16
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: sequence from
: OTHER INFORMATION: a phage display peptide library
US-10-643-465-16

```

Query Match	40.0%;	Score 24;	DB 16;	Length 8;
Best Local Similarity	50.0%;	Pred. No. 1.2e+06;		
Matches	4;	Conservative	1;	Mismatches 3;
			Indels	0;
			Gaps	0;

QY	1	GYKNSKEH	8
Db	1	GYEVQPEH	8

RESULT 3
 US-10-117-937-555
 Sequence 555, Application US/10117937
 Publication No. US2003022039A1
 GENERAL INFORMATION:
 APPLICANT: CTL IMMUNO THERAPIES CORP.
 APPLICANT: SIMARD, John, J.L.
 APPLICANT: DIAMOND, David, C.
 APPLICANT: LIU, Liping
 APPLICANT: XIE, Zhidong
 TITLE OF INVENTION: EPITOPE SEQUENCES
 FILE REFERENCE: CTLMIM.027A
 CURRENT APPLICATION NUMBER: US/10/117,937
 CURRENT FILING DATE: 2002-04-04
 PRIOR APPLICATION NUMBER: US 60/382,211

```

1 PRIOR FILING DATE: 2001-04-06
2 PRIOR APPLICATION NUMBER: US 60/337,017
3 PRIOR FILING DATE: 2001-11-07
4 PRIOR APPLICATION NUMBER: US 60/363,210
5 PRIOR FILING DATE: 2002-03-07
6 NUMBER OF SEQ ID NOS: 602
7 SOFTWARE: FASTSEQ for Windows Version 4.0
8 SEQ ID NO 555
9
10 LENGTH: 9
11
12 TYPE: PR1
13 ORGANISM: Homo sapiens
14
15 US-10-117-937-555

```

Query Match	40.0%;	Score 24;	DB 15;	Length 9;
Best Local Similarity	33.3%;	Pred. No. 1.2e+06;		
Matches	3;	Conservative	3;	Indels 0;
		Mismatches	3;	Gaps 0;

QY	2	YKNSKEHRV	1
			:::
Db	1	YDNKQFEKI	9

```

RESULT 34
US-09-780-053-472
Sequence 472, Application US/09780053
Patent No. US20020102640A1
GENERAL INFORMATION:
APPLICANT: Rene S. Hubert
APPLICANT: Daniel E.H. Afar
APPLICANT: Pia M. Challita-Eid
APPLICANT: Mary Paris
APPLICANT: Elana Lewin
APPLICANT: Steve Chappell Mitchell
APPLICANT: Aya Utkovits
TITLE OF INVENTION: 83P54: A TISSUE SPECIFIC PROTEIN
FILE REFERENCE: 189.SUSU1
CURRENT APPLICATION NUMBER: US/09/780,053
CURRENT FILING DATE: 2001-02-09
PRIORITY FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 716
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 472
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-780-053-472

```

Query Match	40.0%;	Score 24;	DB 9;	Length 10;
Best Local Similarity	57.1%;	Pred. No. 1.1e+03;		
Matches	4;	Conservative	2;	Mismatches 1;
				Indels 0;
				Gaps 0

QY	1	GYKNSKF	7
		::	
Db	4	GHQNSTF	10

```

RESULT 35
US-09-753-126-126
; Sequence 126, Application US/09753126
; Patent No. US20020127219A1
; GENERAL INFORMATION:
; APPLICANT: OKKELS, JENS SIGURD
; APPLICANT: JENSEN, ANNE DAM
; APPLICANT: HALKIER, TORBERN
; APPLICANT: JENSEN, RIKKE BOLDING
; TITLE OF INVENTION: IMPROVED LYSOSOMAL ENZYMES AND LYSOSOMAL ENZYME
; TITLE OF INVENTION: ACTIVATORS
; FILE REFERENCE: 31-0006000US
; CURRENT APPLICATION NUMBER: US/09/753,126
; CURRENT FILING DATE: 2001-06-11
; PRIORITY APPLICATION NUMBER: PA 1999 01891

```

```

; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 60/174,652
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: PA 200 00865
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/210,984
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: 60/211,124
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: PA 2000 01027
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/217,497
; PRIOR FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 126
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-753-126-126
```

```
Query Match          40.0%; Score 24; DB 9; Length 10;
Best Local Similarity 57.1%; Pred.No.1.le+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 YXNSKFH 8
      |||:|
DB      4 YKSYKFY 10
```

```

RESULT 36
US-09-896-896A-90
; Sequence 90, Application US/09896896A
; Publication No. US20030036181A1
; GENERAL INFORMATION:
; APPLICANT: MAXYGEN APS
; TITLE OF INVENTION: PEPTIDE EXTENDED GLYCOSYLATED POLYPEPTIDES
; FILE REFERENCE: 0217u8210
; CURRENT APPLICATION NUMBER: US/09/896,896A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/217,497
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: US 60/225,558
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: DK PA 2000 01027
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DK PA 2000 01092
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: PCT/DK00/00743
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: PCT/DK01/00090
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-896-896A-90
```

```
Query Match          40.0%; Score 24; DB 10; Length 10;
Best Local Similarity 57.1%; Pred.No.1.le+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 YXNSKFH 8
      |||:|
DB      4 YKSYKFY 10
```

```

RESULT 37
US-10-319-340-8
; Sequence 8, Application US/10319340
; Publication No. US20030144211A1
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; APPLICANT: McVeier, Roger P.
; APPLICANT: Geny, Jian-Guo
; TITLE OF INVENTION: Peptide Inhibitors of Inflammation Mediated by Selectins
; FILE REFERENCE: CTC 102 CON DIV
; CURRENT APPLICATION NUMBER: US/10/319,340
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: 06/135,319
; PRIOR FILING DATE: 1993-10-12
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 10
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic inhibitory peptide
US-10-319-340-8
```

```
Query Match          40.0%; Score 24; DB 14; Length 10;
Best Local Similarity 80.0%; Pred.No.1.le+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 YXNSK 6
      |||:|
DB      1 YXNNK 5
```

```

RESULT 38
US-10-117-937-556
; Sequence 556, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: STWARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPIOTOPE SEQUENCES
; FILE REFERENCE: CTILIM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 556
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-556
```

```
Query Match          40.0%; Score 24; DB 15; Length 10;
Best Local Similarity 33.3%; Pred.No.1.le+03;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 YXNSKFH 10
      |||:|
DB      2 YDNKQPEKI 10
```

RESULT 39

US-10-330-697-126
; Sequence 126, Application US/10330697
; Publication No. US20040009165A1
; GENERAL INFORMATION:
; APPLICANT: OKKELS, JENS SIGURD
; APPLICANT: JENSEN, ANNE DAM
; APPLICANT: HALKIER, TORBEN
; APPLICANT: JENSEN, RIKKE BOLDING
; TITLE OF INVENTION: IMPROVED LYSOSOMAL ENZYMES AND LYSOSOMAL ENZYME
; FILE REFERENCE: 31-006000US
; CURRENT APPLICATION NUMBER: US/10/330,697
; CURRENT FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: US/09/753,126
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: PA 1999 01891
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 60/174,652
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: PA 200 00865
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/210,984
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: 60/211,124
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: PA 2000 01027
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/217,497
; PRIOR FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 126
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-330-697-126

Query Match 40.0%; Score 24; DB 15; Length 10;
Best Local Similarity 57.1%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKNSKEH 8
||:|:|:
Db 4 YKSYKFY 10

RESULT 40
US-09-791-393-21
; Sequence 21, Application US/09791393
; Publication No. US20030032200A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; FILE REFERENCE: 2543-1-001 N1
; CURRENT APPLICATION NUMBER: US/09/791,393
; CURRENT FILING DATE: 2002-01-02
; EARLIER APPLICATION NUMBER: GB 0004412.3
; EARLIER FILING DATE: 2000-02-24
; EARLIER APPLICATION NUMBER: GB 0030050.9
; EARLIER FILING DATE: 2000-12-08
; EARLIER APPLICATION NUMBER: US 60/254,830
; EARLIER FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 21
; LENGTH: 11

TYPE: PRT
; ORGANISM: homo sapien
US-09-791-393-21

Query Match 40.0%; Score 24; DB 10; Length 11;
Best Local Similarity 44.4%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYNSKEFR 9
||:|:|:
Db 3 GYNTGYQR 11

RESULT 41
US-09-791-389-21
; Sequence 21, Application US/09791389
; Publication No. US20030032773A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; APPLICANT: Terrett, Jonathan Alexander
; APPLICANT: Tyson, Kerry Louise
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; FILE REFERENCE: 2543-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/791,389
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: GB 0004412.3
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: GB 0030050.9
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/254,830
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 21
; LENGTH: 11
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-389-21

Query Match 40.0%; Score 24; DB 10; Length 11;
Best Local Similarity 44.4%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYNSKEFR 9
||:|:|:
Db 3 GYNTGYQR 11

RESULT 42
US-10-264-309-22
; Sequence 22, Application US/10264309
; Publication No. US20040022794A1
; GENERAL INFORMATION:
; APPLICANT: DURHAM, L. KATHRYN
; APPLICANT: FRIEDMAN, DAVID L.
; APPLICANT: HERATH, HERATH
; APPLICANT: KIMMEL, LIDA H.
; APPLICANT: PAREKH, RAJESH B.
; APPLICANT: POTTER, DAVID M.
; APPLICANT: ROHLF, CHRISTIAN
; APPLICANT: SILBER, B. MICHAEL
; APPLICANT: SNYDER, PETER J.
; APPLICANT: SOARS, HOLLY D.
; APPLICANT: STIGER, THOMAS R.
; APPLICANT: SUNDERLAND, P. TREY
; APPLICANT: TOWNSEND, ROBERT R.
; APPLICANT: WHITE, W. FROST
; APPLICANT: WILLIAMS, STEPHEN A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,

FILE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
FILE REFERENCE: POA-002.01
CURRENT APPLICATION NUMBER: US/10/264,309
CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: 60/326,708
PRIOR FILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 491
SOFTWARE: Patentin Version 2.1
SEQ ID NO 22
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-10-264-309-22

Query Match
Best Local Similarity 40.0%; Score 24; DB 16; Length 11;
Best Local Similarity 44.4%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYKSKFHR 9
Db 3 GYLTNGYOR 11

RESULT 43
US-10-302-100B-12
Sequence 12, Application US/10302100B
Publication No. US20040054131A1
GENERAL INFORMATION:
APPLICANT: Ballinger, Marcus
APPLICANT: Kavanaugh, Michael
TITLE OF INVENTION: Synthetic Peptides Having FGF Receptor
FILE REFERENCE: 035784/263218
CURRENT APPLICATION NUMBER: US/10/302,100B
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: 09/407,687
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: 60/102,667
PRIOR FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 12
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic peptide
US-10-302-100B-12

Query Match
Best Local Similarity 40.0%; Score 24; DB 12; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYKSKFHR 8
Db 5 GYVSCTFH 12

RESULT 44
US-09-734-002-5
Sequence 5, Application US/09734002
Patent No. US2001001633A1
GENERAL INFORMATION:
APPLICANT: Motomaru SEIKI et al.
TITLE OF INVENTION: NOVEL PROTEIN AND MONOCLONAL ANTIBODY SPECIFIC THERETO
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/734,002
FILING DATE: 12-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/01956
FILING DATE: July 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 14
TYPE: Amino acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-734-002-5

Query Match
Best Local Similarity 40.0%; Score 24; DB 9; Length 14;
Best Local Similarity 80.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NSKEH 8
Db 5 SSKFH 9

RESULT 45
US-09-932-613-39
Sequence 39, Application US/09932613
Publication No. US20030091565A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Belter, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: Dlx-025.1 PCT; Dlx-025.1 US
CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: Patentin Version 3.1
SEQ ID NO 39
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-39

Query Match
Best Local Similarity 40.0%; Score 24; DB 10; Length 14;
Best Local Similarity 66.7%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KNSKPH 8
Db 9 KNCKPH 14

Search completed: August 30, 2004, 11:04:56

Thu Sep 2 07:41:37 2004

us-09-720-469a-4.aug30.rapb

Page 13

Job time : 14.4527 secs

Thu Sep 2 07:41:36 2004

us-09-720-469a-4.aug30.rai

Page 1

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CM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:59 ; Search time 4.34797 Seconds
(without alignments)
130.609 Million cell updates/sec

Title: US-09-720-469A-4
Perfect score: 60
Sequence: 1 GYKSKFHRVI 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 78885

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26.5	44.2	11	1	US-08-481-888A-19
2	26.5	44.2	11	1	US-08-485-273A-19
3	26.5	44.2	11	2	US-08-973-563A-19
4	26.5	44.2	11	2	US-08-973-559-19
5	26.5	44.2	11	1	US-08-481-888A-18
6	26.5	44.2	12	1	US-08-485-273A-18
7	26.5	44.2	12	2	US-08-973-563A-18
8	26.5	44.2	12	2	US-08-973-563A-24
9	26.5	44.2	12	2	US-08-973-563A-25
10	26.5	44.2	12	2	US-08-973-563A-37
11	26.5	44.2	12	2	US-08-973-563A-36
12	26.5	44.2	12	2	US-08-973-559-18
13	26.5	44.2	12	2	US-08-973-559-24
14	26.5	44.2	12	2	US-08-973-559-25
15	26.5	44.2	12	2	US-08-973-559-27
16	26.5	44.2	12	2	US-08-973-559-36
17	26.5	44.2	12	3	US-08-993-235-4
18	26.5	44.2	12	3	US-08-993-235-5
19	26.5	44.2	12	3	US-08-993-235-7
20	26.5	44.2	12	4	US-09-226-666-1
21	26.5	44.2	12	4	US-09-226-666-13
22	26.5	44.2	12	4	US-09-226-666-16
23	26.5	44.2	12	4	US-08-993-235-4
24	26.5	44.2	12	4	US-08-993-235-5
25	26.5	44.2	12	4	US-08-993-235-7
26	26.5	44.2	14	1	US-08-287-717-6
27	26.5	44.2	14	1	US-08-481-888A-16

28	26.5	44.2	14	1	US-08-485-273A-16	Sequence 16, Appl
29	26.5	44.2	14	1	US-08-441-914-6	Sequence 6, Appl
30	26.5	44.2	14	2	US-08-973-563A-16	Sequence 16, Appl
31	26.5	44.2	14	2	US-08-973-559-16	Sequence 16, Appl
32	25	41.7	12	1	US-08-511-662-8	Sequence 8, Appl
33	25	41.7	12	5	PCT-US86-12632-8	Sequence 8, Appl
34	24	40.0	8	3	US-08-925-002-16	Sequence 16, Appl
35	24	40.0	8	4	US-09-910-552-16	Sequence 16, Appl
36	24	40.0	9	1	US-08-215-805A-41	Sequence 41, Appl
37	24	40.0	9	4	US-09-417-608A-86	Sequence 86, Appl
38	24	40.0	10	1	US-07-909-122-5	Sequence 5, Appl
39	24	40.0	10	4	US-08-135-919A-8	Sequence 8, Appl
40	24	40.0	11	1	US-08-269-441A-3	Sequence 3, Appl
41	24	40.0	12	4	US-09-446-787B-88	Sequence 88, Appl
42	24	40.0	12	4	US-09-407-687-12	Sequence 12, Appl
43	24	40.0	13	2	US-08-480-190-229	Sequence 229, App
44	24	40.0	13	2	US-08-488-379-229	Sequence 229, App
45	24	40.0	13	4	US-08-475-399A-229	Sequence 229, App

ALIGNMENTS

RESULT 1
US-08-481-888A-19
Sequence 19, Application US/08481888A
Patent No. 5631228
GENERAL INFORMATION:
APPLICANT: Oppenheim, Frank G.
APPLICANT: Xu, Tao
TITLE OF INVENTION: ANTI-FUNGAL AND ANTI-BACTERIAL
TITLE OF INVENTION: HISTATIN-BASED PEPTIDES
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,888A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/287,717
FILING DATE: 09-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,030
FILING DATE: 28-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/786,571
FILING DATE: 01-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: PER95-01A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-481-888A-19

Query Match 44.2%; Score 26.5; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 1e+02; 1;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKSKFH 8
||| |||
5 GYKR-KFH 11

RESULT 2
US-08-485-273A-19

; Sequence 19, Application US/08485273A
; Patent No. 5646119

GENERAL INFORMATION:

APPLICANT: Oppenheim, Frank G.

APPLICANT: Xu, Tao

APPLICANT: Spacciapoli, Peter

TITLE OF INVENTION: D-Amino Acid Histatin-Based Peptides as

TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial Agents

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Millitia Drive

CITY: Lexington

STATE: MA

COUNTRY: US

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,273A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/287,717

FILING DATE: 09-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/145,030

FILING DATE: 28-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/786,571

FILING DATE: 01-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: Brook, David E.

REGISTRATION NUMBER: 22,592

REFERENCE/DOCKET NUMBER: PER95-02A

TELEPHONE: 617-861-6240

TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Region

LOCATION: 1..11

OTHER INFORMATION: /note= "At least one amino acid

US-08-485-273A-19

Query Match 44.2%; Score 26.5; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 1e+02; 1;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKSKFH 8

Db 5 GYKR-KFH 11

RESULT 3
US-08-973-563A-19
; Sequence 19, Application US/08973563A
; Patent No. 5885965

GENERAL INFORMATION:

APPLICANT: Oppenheim, Frank G.

APPLICANT: Xu, Tao

APPLICANT: Spacciapoli, Peter

APPLICANT: Roberts, F. D.

APPLICANT: Friden, Philip M.

TITLE OF INVENTION: Anti-Fungal D-Amino Acid Histatin-Based

TITLE OF INVENTION: Peptides

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Millitia Drive

CITY: Lexington

STATE: MA

COUNTRY: US

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/973,563A

FILING DATE: 07-JUN-1996

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/485,273

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Brook, David E.

REGISTRATION NUMBER: 22,592

REFERENCE/DOCKET NUMBER: PER95-02A2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 781-861-6240

TELEFAX: 781-861-9540

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Region

LOCATION: 1..11

OTHER INFORMATION: /note= "At least one amino acid

US-08-973-563A-19

Query Match 44.2%; Score 26.5; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 1e+02; 1;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKSKFH 8
||| |||
5 GYKR-KFH 11

RESULT 4
US-08-973-559-19

; Sequence 19, Application US/08973559
; Patent No. 5912230

GENERAL INFORMATION:

APPLICANT: OPPENHEIM, FRANK G.

APPLICANT: XU, TAO

APPLICANT: ROBERTS, F. D.
APPLICANT: SPACIAPOLI, PETER
APPLICANT: FRIDEN, PHILIP M.
TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial
TITLE OF INVENTION: Histatin-Based Peptides
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,559
FILING DATE: 07-JUN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,888
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: PER95-01A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-973-559-19

Query Match 44.2%; Score 26.5; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 1e+02; 1; Indels 1; Gaps 1;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKSKKFH 8
DB 5 GYKR-KFH 11

RESULT 5
US-08-481-888A-18
Sequence 18, Application US/08481888A
Patent No. 5631228
GENERAL INFORMATION:
APPLICANT: Oppenheim, Frank G.
APPLICANT: Xu, Tao
APPLICANT: Roberts, F. Donald
TITLE OF INVENTION: ANTI-FUNGAL AND ANTI-BACTERIAL
TITLE OF INVENTION: HISTATIN-BASED PEPTIDES
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,888A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/287,717
FILING DATE: 09-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,030
FILING DATE: 28-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/786,571
FILING DATE: 01-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: PER95-01A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-481-888A-18

Query Match 44.2%; Score 26.5; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+02; 1; Indels 1; Gaps 1;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKSKKFH 8
DB 6 GYKR-KFH 12

RESULT 6
US-08-485-273A-18
Sequence 18, Application US/08485273A
Patent No. 5646119
GENERAL INFORMATION:
APPLICANT: Oppenheim, Frank G.
APPLICANT: Xu, Tao
APPLICANT: Spaciapoli, Peter
TITLE OF INVENTION: D-Amino Acid Histatin-Based Peptides as
TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial Agents
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,273A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/287,717
FILING DATE: 09-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,030
FILING DATE: 28-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/786,571

FILING DATE: 01-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: PER95-02A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 1..12
OTHER INFORMATION: /note= "At least one amino acid
US-08-485-273A-18
must have a D configuration."

Query Match 44.2% Score 26.5; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKSKFH 8
DB 6 GYK-R-KFH 12

RESULT 7
US-08-973-563A-18
Sequence 18, Application US/08973563A
Patent No. 5885965
GENERAL INFORMATION:
APPLICANT: Oppenheim, Frank G.
APPLICANT: Xu, Tao
APPLICANT: Spacciapoli, Peter
APPLICANT: Roberts, F. D.
APPLICANT: Friden, Philip M.
TITLE OF INVENTION: Anti-Fungal D-Amino Acid Histatin-Based
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,563A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,273
FILING DATE: 07-JUN-1995
REFERENCE/DOCKET NUMBER: PER95-02A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids

TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 1..12
OTHER INFORMATION: /note= "At least one amino acid
US-08-973-563A-18
must have a D configuration."

Query Match 44.2% Score 26.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKSKFH 8
DB 6 GYK-R-KFH 12

RESULT 8
US-08-973-563A-24
Sequence 24, Application US/08973563A
Patent No. 5885965
GENERAL INFORMATION:
APPLICANT: Oppenheim, Frank G.
APPLICANT: Xu, Tao
APPLICANT: Spacciapoli, Peter
APPLICANT: Roberts, F. D.
APPLICANT: Friden, Philip M.
TITLE OF INVENTION: Anti-Fungal D-Amino Acid Histatin-Based
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,563A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,273
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: PER95-02A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 1..12
OTHER INFORMATION: /note= "At least one amino acid
US-08-973-563A-24
must have a D configuration."

Query Match 44.2%; Score 26.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 GYKSKFH 8
DB 6 GYKR-KFH 12

RESULT 9
US-08-973-563A-25
Sequence 25, Application US/08973563A
Patent No. 5885965
GENERAL INFORMATION:
APPLICANT: Oppenheim, Frank G.
APPLICANT: Xu, Tao
APPLICANT: Spacciapoli, Peter
APPLICANT: Roberts, F. D.
APPLICANT: Friden, Philip M.
TITLE OF INVENTION: Anti-Fungal D-Amino Acid Histatin-Based
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,563A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,273
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: PER95-02A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 1..12
OTHER INFORMATION: /note="At least one amino acid
OTHER INFORMATION: must have a D configuration."

Query Match 44.2%; Score 26.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 GYKSKFH 8
DB 6 GYKR-KFH 12

RESULT 10
US-08-973-563A-27

Sequence 27, Application US/08973563A
Patent No. 5885965
GENERAL INFORMATION:
APPLICANT: Oppenheim, Frank G.
APPLICANT: Xu, Tao
APPLICANT: Spacciapoli, Peter
APPLICANT: Roberts, F. D.
APPLICANT: Friden, Philip M.
TITLE OF INVENTION: Anti-Fungal D-Amino Acid Histatin-Based
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,563A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,273
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: PER95-02A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 1..12
OTHER INFORMATION: /note="At least one amino acid
OTHER INFORMATION: must have a D configuration."

US-08-973-563A-27

Query Match 44.2%; Score 26.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 GYKSKFH 8
DB 6 GYKR-KFH 12

RESULT 11
US-08-973-563A-36
Sequence 36, Application US/08973563A
Patent No. 5885965
GENERAL INFORMATION:
APPLICANT: Oppenheim, Frank G.
APPLICANT: Xu, Tao
APPLICANT: Spacciapoli, Peter
APPLICANT: Roberts, F. D.
APPLICANT: Friden, Philip M.
TITLE OF INVENTION: Anti-Fungal D-Amino Acid Histatin-Based
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 37

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
;; STREET: Two Militia Drive
;; CITY: Lexington
;; STATE: MA
;; COUNTRY: US
;; ZIP: 02173
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/973,563A
;; FILING DATE: 07-JUN-1996
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/485,273
;; FILING DATE: 07-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Brook, David E.
;; REGISTRATION NUMBER: 22,592
;; REFERENCE/DOCKET NUMBER: PER95-02A2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 781-861-9540
;; TELEFAX: 781-861-9540
;; INFORMATION FOR SEQ ID NO: 36:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 12 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Region
;; LOCATION: 1..12
;; OTHER INFORMATION: /note="At least one amino acid
;; OTHER INFORMATION: must have a D configuration."
;;
;; US-08-973-563A-36
;;
Query Match 44.2%; Score 26.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
;;
QY 1 GYKSKFPH 8
Db 6 GYK-QKPH 12
;;
RESULT 12
;; US-08-973-559-18
;; Sequence 18, Application US/08973559
;; Patent No. 5912230
;; GENERAL INFORMATION:
;; APPLICANT: OPPENHEIM, FRANK G.
;; APPLICANT: XU, TAO
;; APPLICANT: ROBERTS, F. D.
;; APPLICANT: SPACCIAPOLI, PETER
;; APPLICANT: FRIDEN, PHILIP M.
;; TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial
;; TITLE OF INVENTION: Histatin-Based Peptides
;; NUMBER OF SEQUENCES: 37
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
;; STREET: Two Militia Drive
;; CITY: Lexington
;; STATE: MA
;; COUNTRY: US
;; ZIP: 02173
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/973,559
;; FILING DATE: 07-JUN-1996
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/481,888
;; FILING DATE: 07-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Brook, David E.
;; REGISTRATION NUMBER: 22,592
;; REFERENCE/DOCKET NUMBER: PER95-01A2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 781-861-6240
;; TELEFAX: 781-861-9540
;; INFORMATION FOR SEQ ID NO: 18:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 12 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;;
;; US-08-973-559-18
;;
Query Match 44.2%; Score 26.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
;;
QY 1 GYKSKFPH 8
Db 6 GYK-QKPH 12
;;
RESULT 13
;; US-08-973-559-24
;; Sequence 24, Application US/08973559
;; Patent No. 5912230
;; GENERAL INFORMATION:
;; APPLICANT: OPPENHEIM, FRANK G.
;; APPLICANT: XU, TAO
;; APPLICANT: ROBERTS, F. D.
;; APPLICANT: SPACCIAPOLI, PETER
;; APPLICANT: FRIDEN, PHILIP M.
;; TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial
;; TITLE OF INVENTION: Histatin-Based Peptides
;; NUMBER OF SEQUENCES: 37
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
;; STREET: Two Militia Drive
;; CITY: Lexington
;; STATE: MA
;; COUNTRY: US
;; ZIP: 02173
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/973,559
;; FILING DATE: 07-JUN-1996
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/481,888
;; FILING DATE: 07-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Brook, David E.
;; REGISTRATION NUMBER: 22,592
;; REFERENCE/DOCKET NUMBER: PER95-01A2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 781-861-6240
;; TELEFAX: 781-861-9540
;; INFORMATION FOR SEQ ID NO: 24:

Thu Sep 2 07:41:36 2004

us-09-720-469a-4.aug30.rai

Page 7

SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-973-559-24

Query Match 44.2%; Score 26.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKSKFH 8
DB 6 GYKR-KFH 12

RESULT 14
US-08-973-559-25
Sequence 25, Application US/08973559
Patent No. 5912230
GENERAL INFORMATION:
APPLICANT: OPPENHEIM, FRANK G.
APPLICANT: XU, TAO
APPLICANT: ROBERTS, F. D.
APPLICANT: SPACCIAPOLI, PETER
APPLICANT: FRIDEN, PHILIP M.
TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial
TITLE OF INVENTION: Histatin-Based Peptides
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,559
FILING DATE: 07-JUN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,888
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: PER95-01A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-973-559-25

Query Match 44.2%; Score 26.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKSKFH 8
DB 6 GYKR-KFH 12

RESULT 15
US-08-973-559-27
Sequence 27, Application US/08973559
Patent No. 5912230
GENERAL INFORMATION:
APPLICANT: OPPENHEIM, FRANK G.
APPLICANT: XU, TAO
APPLICANT: ROBERTS, F. D.
APPLICANT: SPACCIAPOLI, PETER
APPLICANT: FRIDEN, PHILIP M.
TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial
TITLE OF INVENTION: Histatin-Based Peptides
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,559
FILING DATE: 07-JUN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,888
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: PER95-01A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-973-559-27

Query Match 44.2%; Score 26.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKSKFH 8
DB 6 GYKR-KFH 12

RESULT 16
US-08-973-559-36
Sequence 36, Application US/08973559
Patent No. 5912230
GENERAL INFORMATION:
APPLICANT: OPPENHEIM, FRANK G.
APPLICANT: XU, TAO
APPLICANT: ROBERTS, F. D.
APPLICANT: SPACCIAPOLI, PETER
APPLICANT: FRIDEN, PHILIP M.
TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial
TITLE OF INVENTION: Histatin-Based Peptides
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: TWO MILLITIA DRIVE
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,559
FILING DATE: 07-JUN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,888
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: PER95-01A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-973-559-36

Query Match 44.2%; Score 26.5; DB 3; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKSKFH 8
DB 6 GYK-KFH 12

RESULT 17
US-08-993-235-4
Sequence 4, Application US/08993235
Patent No. 6084064
GENERAL INFORMATION:
APPLICANT: OPPENHEIM, FRANK G.
APPLICANT: ROBERTS, F. DONALD
APPLICANT: XU, TAO
TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES
FILE REFERENCE: 50032/002001
CURRENT APPLICATION NUMBER: US/08/993,235
CURRENT FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
US-08-993-235-4

Query Match 44.2%; Score 26.5; DB 3; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKSKFH 8
DB 6 GYK-KFH 12

RESULT 18

US-08-993-235-5
Sequence 5, Application US/08993235
Patent No. 6084064
GENERAL INFORMATION:
APPLICANT: OPPENHEIM, FRANK G.
APPLICANT: ROBERTS, F. DONALD
APPLICANT: XU, TAO
TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES
FILE REFERENCE: 50032/002001
CURRENT APPLICATION NUMBER: US/08/993,235
CURRENT FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
US-08-993-235-5

Query Match 44.2%; Score 26.5; DB 3; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKSKFH 8
DB 6 GYK-KFH 12

RESULT 19
US-08-993-235-7
Sequence 7, Application US/08993235
Patent No. 6084064
GENERAL INFORMATION:
APPLICANT: OPPENHEIM, FRANK G.
APPLICANT: ROBERTS, F. DONALD
APPLICANT: XU, TAO
TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES
FILE REFERENCE: 50032/002001
CURRENT APPLICATION NUMBER: US/08/993,235
CURRENT FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
US-08-993-235-7

Query Match 44.2%; Score 26.5; DB 3; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKSKFH 8
DB 6 GYK-KFH 12

RESULT 20
US-09-226-666-1
Sequence 1, Application US/09226666A
Patent No. 6528488
GENERAL INFORMATION:
APPLICANT: Spaccapoli, Peter
APPLICANT: Rotstein, David M.
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: METHOD FOR TREATING CYSTIC FIBROSIS
FILE REFERENCE: 50032/007001
CURRENT APPLICATION NUMBER: US/09/226,666A
CURRENT FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Internal fragment
US-09-226-666-1

Query Match 44.2%; Score 26.5; DB 4; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKSKFH 8
DB 6 GYKR-KFH 12

RESULT 21
US-09-226-666-13
Sequence 13, Application US/09226666A
Patent No. 6528488
GENERAL INFORMATION:
APPLICANT: Spacciapoli, Peter
APPLICANT: Rotenstein, David M.
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: METHOD FOR TREATING CYSTIC FIBROSIS
FILE REFERENCE: 50032/007001
CURRENT APPLICATION NUMBER: US/09/226,666A
CURRENT FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Derived from Homo sapiens
US-09-226-666-13

Query Match 44.2%; Score 26.5; DB 4; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKSKFH 8
DB 6 GYKR-KFH 12

RESULT 22
US-09-226-666-16
Sequence 16, Application US/09226666A
Patent No. 6528488
GENERAL INFORMATION:
APPLICANT: Spacciapoli, Peter
APPLICANT: Rotenstein, David M.
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: METHOD FOR TREATING CYSTIC FIBROSIS
FILE REFERENCE: 50032/007001
CURRENT APPLICATION NUMBER: US/09/226,666A
CURRENT FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Derived from Homo sapiens
US-09-226-666-16

Query Match 44.2%; Score 26.5; DB 4; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKSKFH 8
DB 6 GYKR-KFH 12

RESULT 23
US-08-993-235-4
Sequence 4, Application US/08993235
Patent No. 6531573
GENERAL INFORMATION:
APPLICANT: OPPENHEIM, FRANK G.
APPLICANT: ROBERTS, F. DONALD
APPLICANT: XU, TAO
TITLE OF INVENTION: ANTI-FUNGAL AND ANTI-BACTERIAL PEPTIDES
FILE REFERENCE: 50032/002001
CURRENT APPLICATION NUMBER: US/08/993,235
CURRENT FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
US-08-993-235-4

Query Match 44.2%; Score 26.5; DB 4; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKSKFH 8
DB 6 GYKR-KFH 12

RESULT 24
US-08-993-235-5
Sequence 5, Application US/08993235
Patent No. 6531573
GENERAL INFORMATION:
APPLICANT: OPPENHEIM, FRANK G.
APPLICANT: ROBERTS, F. DONALD
APPLICANT: XU, TAO
TITLE OF INVENTION: ANTI-FUNGAL AND ANTI-BACTERIAL PEPTIDES
FILE REFERENCE: 50032/002001
CURRENT APPLICATION NUMBER: US/08/993,235
CURRENT FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
US-08-993-235-5

Query Match 44.2%; Score 26.5; DB 4; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKSKFH 8
DB 6 GYKR-KFH 12

RESULT 25
US-08-993-235-7
Sequence 7, Application US/08993235
Patent No. 6531573
GENERAL INFORMATION:
APPLICANT: OPPENHEIM, FRANK G.
APPLICANT: ROBERTS, F. DONALD

APPLICANT: XU, TAO
APPLICANT: SPACCIAPOLI, PETER
TITLE OF INVENTION: ANTI-FUNGAL AND ANTI-BACTERIAL PEPTIDES
FILE REFERENCE: 50032/002001
CURRENT APPLICATION NUMBER: US/08/993,235
CURRENT FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
US-08-993-235-7

Query Match 44.2%; Score 26.5; DB 1; Length 14;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKSKFH 8
DB 6 GYKR-KFH 12

RESULT 26
US-08-287-717-6
Sequence 6, Application US/08287717
Patent No. 5486503
GENERAL INFORMATION:
APPLICANT: Oppenheim, Frank G.
TITLE OF INVENTION: No. 5486503e1 Anti-Fungal Peptides and Uses
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/287,717
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/145,030
FILING DATE:
APPLICATION NUMBER: US 07/786,571
FILING DATE: 01-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: BU91-17
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-287-717-6

Query Match 44.2%; Score 26.5; DB 1; Length 14;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKSKFH 8
DB 1 GYKR-KFH 7

RESULT 27
US-08-481-888A-16
Sequence 16, Application US/08481888A
Patent No. 5631228
GENERAL INFORMATION:
APPLICANT: Oppenheim, Frank G.
APPLICANT: Xu, Tao
TITLE OF INVENTION: ANTI-FUNGAL AND ANTI-BACTERIAL
TITLE OF INVENTION: HISTATIN-BASED PEPTIDES
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,888A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/287,717
FILING DATE: 09-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,030
FILING DATE: 28-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/786,571
FILING DATE: 01-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: PER95-01A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-481-888A-16

Query Match 44.2%; Score 26.5; DB 1; Length 14;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKSKFH 8
DB 1 GYKR-KFH 7

RESULT 28
US-08-485-273A-16
Sequence 16, Application US/08485273A
Patent No. 5646119
GENERAL INFORMATION:
APPLICANT: Oppenheim, Frank G.
APPLICANT: Xu, Tao

APPLICANT: Spacciapoli, Peter
TITLE OF INVENTION: D-Amino Acid Histatin-Based Peptides as
TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial Agents
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,273A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/287,717
FILING DATE: 09-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,030
FILING DATE: 28-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/786,571
FILING DATE: 01-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: PER95-02A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-9540
TELEFAX: 617-861-6240
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 1..14
OTHER INFORMATION: /note="at least one amino acid
must have a D configuration."
US-08-485-273A-16

Query Match 44.2%; Score 26.5; DB 1; Length 14;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 GYKSKFH 8
Db 1 GYKR-KFH 7
RESULT 29
US-08-441-914-6
Sequence 6, Application US/08441914
Patent No. 5636078
GENERAL INFORMATION:
APPLICANT: Oppenheim, Frank G.
APPLICANT: Xu, Tao
TITLE OF INVENTION: No. 5636078el Anti-Fungal Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington

STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,914
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/287,717
FILING DATE: 09-AUG-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/145,030
FILING DATE: 28-OCT-93
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/786,571
FILING DATE: 01-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: David E. Brook
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: BU91-17P22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-441-914-6

Query Match 44.2%; Score 26.5; DB 1; Length 14;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 GYKSKFH 8
Db 1 GYKR-KFH 7
RESULT 30
US-08-973-563A-16
Sequence 16, Application US/08973563A
Patent No. 5885965
GENERAL INFORMATION:
APPLICANT: Oppenheim, Frank G.
APPLICANT: Xu, Tao
APPLICANT: Spacciapoli, Peter
APPLICANT: Roberts, F. D.
APPLICANT: Friden, Philip M.
TITLE OF INVENTION: Anti-Fungal D-Amino Acid Histatin-Based
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,563A
FILING DATE: 07-JUN-1996

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,273
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: PER95-02A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 1..14
OTHER INFORMATION: /note="At least one amino acid
US-08-973-563A-16 must have a D configuration."

Query Match 44.2%; Score 26.5; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 GYKSKFH 8
Db 1 GYK-R-KFH 7

RESULT 31
US-08-973-559-16
Sequence 16, Application US/08973559
Patent No. 5912230
GENERAL INFORMATION:
APPLICANT: OPPENHEIM, FRANK G.
APPLICANT: XU, TAO
APPLICANT: ROBERTS, F. D.
APPLICANT: SPACCIAPOLI, PETER
APPLICANT: FRIDEN, PHILIP M.
TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial
TITLE OF INVENTION: Histatin-Based Peptides
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,559
FILING DATE: 07-JUN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,888
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: PER95-01A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540

INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-973-559-16

Query Match 44.2%; Score 26.5; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 GYKSKFH 8
Db 1 GYK-R-KFH 7

RESULT 32
US-08-511-662-8
Sequence 8, Application US/08511662
Patent No. 5807552
GENERAL INFORMATION:
APPLICANT: Stanton, G. John
APPLICANT: Hughes, Jr., Thomas K.
TITLE OF INVENTION: Compositions for Confering Immunogenicity
TITLE OF INVENTION: to a Substance and Uses Thereof
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,662
FILING DATE: Concurrently herewith
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Hodgins, Daniel S.
REGISTRATION NUMBER: 31,026
REFERENCE/DOCKET NUMBER: UTSG:162/HOD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515/418-3000
TELEFAX: 512/474-7577
TELEX: NA
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-511-662-8

Query Match 41.7%; Score 25; DB 1; Length 12;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YKSKFH 8
Db 5 YKMRFH 11

RESULT 33
PCT-US96-12632-8

Sequence 8, Application FC/TUS9612632
GENERAL INFORMATION:
APPLICANT: NAME: BOARD OF REGENTS, THE UNIVERSITY OF
APPLICANT: TEXAS SYSTEM
APPLICANT: STREET: 201 West 7th Street
APPLICANT: CITY: Austin
APPLICANT: STATE: Texas
APPLICANT: COUNTRY: United States of America
APPLICANT: POSTAL CODE: 78701
APPLICANT: TELEPHONE NO: (512) 499-4462
APPLICANT: TELEFAX: (512) 499-4523
TITLE OF INVENTION: COMPOSITIONS FOR CONFERRING
TITLE OF INVENTION: IMMUNOGENICITY TO A SUBSTANCE AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12632
FILING DATE: CONCURRENTLY HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US96/08/511,662
FILING DATE: 04 August 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: HODGINS, DANIEL S.
REGISTRATION NUMBER: 31,026
REFERENCE/DOCKET NUMBER: UFG162P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515/418-3000
TELEFAX: 512/474-7577
TELEX: NA
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: peptide
PCT-US96-12632-8
Query Match 41.7%; Score 25; DB 5; Length 12;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YNKSKEH 8
Db 5 YNLSRFH 11

RESULT 34
US-08-925-002-16
Sequence 16, Application US/08925002
GENERAL INFORMATION:
APPLICANT: Granoff, Dan M.
APPLICANT: Moe, Gregory R.
TITLE OF INVENTION: USE OF MONOCLONAL ANTIBODIES THAT DEFINE UNIQUE
TITLE OF INVENTION: MENINGOCOCCAL B EPITOPES IN THE PREPARATION OF VACCINE
FILE REFERENCE: 1238.002

CURRENT APPLICATION NUMBER: US/08/925,002
CURRENT FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: sequence from
US-08-925-002-16
Query Match 40.0%; Score 24; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYKSKFH 8
Db 1 GYEVQPFH 8

RESULT 35
US-09-910-552-16
Sequence 16, Application US/09910552
Patent No. 6642354
GENERAL INFORMATION:
APPLICANT: Moe, Gregory R.
APPLICANT: Granoff, Dan M.
TITLE OF INVENTION: USE OF MONOCLONAL ANTIBODIES THAT DEFINE UNIQUE
TITLE OF INVENTION: MENINGOCOCCAL B EPITOPES IN THE PREPARATION OF VACCINE
FILE REFERENCE: 1238.002
CURRENT APPLICATION NUMBER: US/09/910,552
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: 09/494,822
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: sequence from
US-09-910-552-16
Query Match 40.0%; Score 24; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYKSKFH 8
Db 1 GYEVQPFH 8

RESULT 36
US-08-215-805A-41
Sequence 41, Application US/08215805A
Patent No. 5559008
GENERAL INFORMATION:
APPLICANT: Chang, Yung-Fu
TITLE OF INVENTION: LEUKOTOXIN GENE FROM PASTURELLA
TITLE OF INVENTION: SUTS
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/215,805A
FILING DATE: 22-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/61 (D-1329A)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Actinobacillus pleuropneumoniae
US-08-215-805A-41

Query Match 40.0%; Score 24; DB 1; Length 9;
Best Local Similarity 44.4%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 YKSKFHRV 10
: |||:
Db 1 FKSKFRDI 9

RESULT 37
US-09-417-608A-86
; Sequence 86, Application US/09417608A
; Patent No. 6686164
; GENERAL INFORMATION:
; APPLICANT: Olsen, Arne
; APPLICANT: Roggen, Erwin
; APPLICANT: Ernst, Steffen
; TITLE OF INVENTION: Low Allergenic Protein Variants
; FILE REFERENCE: 5676.200-US
; CURRENT APPLICATION NUMBER: US/09/417,608A
; CURRENT FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: Patentin version 3.2
; SEQ ID NO: 86
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-417-608A-86

Query Match 40.0%; Score 24; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKSKF 7
: |||:
Db 3 FSNKRF 8

RESULT 38
US-07-909-122-5
; Sequence 5, Application US/07909122
; Patent No. 5415995
; GENERAL INFORMATION:
; APPLICANT: SCHOOLNIK, GARY K.

APPLICANT: PALEFSKY, JOEL M.
TITLE OF INVENTION: DIAGNOSTIC PEPTIDES OF HUMAN PAPILLOMA
VIRUS
TITLE OF INVENTION: VIRUS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/909,122
FILING DATE: 19920706
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: BENZ, WILLIAM H.
REGISTRATION NUMBER: 25,952
REFERENCE/DOCKET NUMBER: 28600-20105.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-909-122-5

Query Match 40.0%; Score 24; DB 1; Length 10;
Best Local Similarity 37.5%; Pred. No. 2.6e+02;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 KNSKFRHV 10
: |||:
Db 2 KKQRFHNI 9

RESULT 39
US-08-135-319A-8
; Sequence 8, Application US/08135319A
; Patent No. 6528487
; GENERAL INFORMATION:
; APPLICANT: Heavener, George A.
; APPLICANT: McEwen, Roger P.
; APPLICANT: Geng, Jian-Guo
; TITLE OF INVENTION: Peptide Inhibitors of Inflammation Mediated by Selectins
; FILE REFERENCE: CTC 102 CON
; CURRENT APPLICATION NUMBER: US/08/135,319A
; CURRENT FILING DATE: 1993-10-12
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 8
; LENGTH: 10
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic inhibitory peptide
US-08-135-319A-8

Query Match 40.0%; Score 24; DB 4; Length 10;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKSK 6
: |||:

DB 1 YKXNK 5

RESULT 40
US-08-269-441A-3
Sequence 3, Application US/08269441A
Patent No. 5552529
GENERAL INFORMATION:
APPLICANT: Rearden, Ann
TITLE OF INVENTION: A NOVEL AUTOANTIGEN, PINCH
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/269,441A
FILING DATE: 30-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haile Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07257/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..11
US-08-269-441A-3

Query Match 40.0%; Score 24; DB 1; Length 11;
Best Local Similarity 42.9%; Pred. No. 2.8e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 YKXSKFH 8
: || :
DB 1 PKNDPYH 7

RESULT 41
US-09-446-787B-88
Sequence 88, Application US/09446787B
Patent No. 6541198
GENERAL INFORMATION:
APPLICANT: Akzo No. 6541198el N.V.
APPLICANT: Paulij, Wilhemina P.
APPLICANT: Van Kessel-Koenen, Marjolijn J.
TITLE OF INVENTION: Antibodies and other binding molecules specific for hepatitis B v
FILE REFERENCE: 9310-19
CURRENT APPLICATION NUMBER: US/09/446,787B
CURRENT FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patent version 3.1
SEQ ID NO 88
LENGTH: 12
TYPE: PRT

ORGANISM: Hepatitis B virus
US-09-446-787B-88

Query Match 40.0%; Score 24; DB 4; Length 12;
Best Local Similarity 30.0%; Pred. No. 3.1e+02;
Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 YKXSKFHVI 11
: || :
DB 3 WNSTFHQVL 12

RESULT 42
US-09-407-687-12
Sequence 12, Application US/09407687
Patent No. 6548634
GENERAL INFORMATION:
APPLICANT: Ballinger, Marcus
APPLICANT: Kavanaugh, Michael
TITLE OF INVENTION: Synthetic Peptides Having FGF Receptor
FILE REFERENCE: 1517.001
CURRENT APPLICATION NUMBER: US/09/407,687
CURRENT FILING DATE: 1999-09-28
EARLIER APPLICATION NUMBER: 60/102,667
EARLIER FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 12
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic peptide
US-09-407-687-12

Query Match 40.0%; Score 24; DB 4; Length 12;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXSKTFH 8
: || :
DB 5 GYXSKTFH 12

RESULT 43
US-08-480-190-229
Sequence 229, Application US/08480190
Patent No. 5627516
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,190
FILING DATE:

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 229:
SEQUENCE CHARACTERISTICS:
LENGTH: 13
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-480-190-229

Query Match 40.0%; Score 24; DB 2; Length 13;
Best Local Similarity 44.4%; Pred. No. 3.4e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 YKNSKPHRV 10
| : | : | :
Db 5 YRGSTSHRL 13

RESULT 44
US-08-488-379-229
Sequence 229, Application US/08488379
Patent No. 5880103
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,379
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154

INFORMATION FOR SEQ ID NO: 229:
SEQUENCE CHARACTERISTICS:
LENGTH: 13
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-488-379-229

Query Match 40.0%; Score 24; DB 2; Length 13;
Best Local Similarity 44.4%; Pred. No. 3.4e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 YKNSKPHRV 10
| : | : | :
Db 5 YRGSTSHRL 13

RESULT 45
US-08-475-399A-229
Sequence 229, Application US/08475399A
Patent No. 6509033
GENERAL INFORMATION:
APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
APPLICANT: Vignali, Dario A.A.
APPLICANT: Hedley, Mary L.
APPLICANT: Stern, Lawrence J.
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 276
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,399A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: 15-JUN-1993
APPLICATION NUMBER: 07/925,460
FILING DATE: 11-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00246/168003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-507
TELEFAX: 617/542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO: 229:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-475-399A-229

Query Match 40.0%; Score 24; DB 4; Length 13;
Best Local Similarity 44.4%; Pred. No. 3.4e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 YKNSKPHRV 10
| : | : | :
Db 5 YRGSTSHRL 13

Thu Sep 2 07:41:36 2004

Search completed: August 30, 2004, 10:57:13
JOD time : 5.34797 secs

us-09-720-469a-4.aug30.rat

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:34 ; Search time 10.5912 Seconds
(without alignments)
327.696 Million cell updates/sec

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Title: US-09-720-469A-5
Perfect score: 71
Sequence: 1 NFKLKHYGPW 11
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Searched:      1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 3347

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Minimum DB seq length: 8
Maximum DB seq length: 14
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```

1:  sp. archaea: *
2:  sp. bacteria: *
3:  sp. fungi: *
4:  sp. innaaa: *
5:  sp. invertebrate: *
6:  sp. mammal: *
7:  sp. mhc: *
8:  sp. organelle: *
9:  sp. phase: *
10: sp. plant: *
11: sp. rodent: *
12: sp. virus: *
13: sp. vertebrate: *
14: sp. unclassified: *
15: sp. virus: *
16: sp. bacteria: *
17: sp. archaea: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	26	36	6	10	11	Q9QVE9 mus sp. pro
2	26	36	6	12	10	Q93XV8 nicotiana t
3	24	33	8	9	4	Q9H3Z6 homo sapien
4	24	33	8	9	13	Q9P374 lepisosteus
5	24	33	8	12	8	Q9XVR6
6	24	33	8	12	8	Q9XVR6
7	24	33	8	12	15	Q12030 caprine art
8	24	33	8	12	15	Q12094 caprine art
9	24	33	8	12	15	Q12114 caprine art
10	24	33	8	12	15	Q12106 caprine art
11	24	33	8	12	15	Q12092 caprine art
12	24	33	8	12	15	Q12108 caprine art
13	24	33	8	12	15	Q12074 caprine art
14	24	33	8	12	15	Q12116 caprine art
15	24	33	8	12	15	Q12118 caprine art
16	24	33	8	12	15	Q12110 caprine art

[illegible]

ALIGNMENTS

[illegible]

```

DE Putative coat protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Nicotiana.
OC NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RA van der Winden J.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20027532; PubMed=10557305;
RA Jakovitsch J.; Merte M.F.; van der Winden J.; Matzke M.A.;
RA Matzke A.J.;
RT "Integrated pararetroviral sequences define a unique class of
RT dispersed repetitive DNA in plants.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:13241-13246(1999).
DR EMBL; AJ41170; CAC88799.1;
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; P:Structural molecule activity; IEA.
KM Coat protein.
FT NON_TER
SQ SEQUENCE 12 AA; 1402 MW; 89226B3A0351E321 CRC64;

Query Match
Best Local Similarity 36.6%; Score 26; DB 10; Length 12;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KHVG 8
DB 6 KHVG 9

RESULT 3
Q9H326 PRELIMINARY; PRT; 9 AA.
ID Q9H326;
AC Q9H326;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE NAD+-dependent isocitrate dehydrogenase 3 alpha subunit
DE (Fragment).
GN IDH3A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim Y.-O.; Koh H.-J.; Jo S.-H.; Son M.-K.; Huh T.-L.;
RT "Structural and functional characterization of the human NAD+-
RT dependent isocitrate dehydrogenase alpha subunit promoter.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157515; AAG43379.1;
FT NON_TER
SQ SEQUENCE 9 AA; 960 MW; C91CB0437DC7687D CRC64;

Query Match
Best Local Similarity 33.8%; Score 24; DB 4; Length 9;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 GPGW 11
DB 3 GPGW 6

RESULT 4
Q9PRJ4 PRELIMINARY; PRT; 9 AA.
ID Q9PRJ4;
AC Q9PRJ4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

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DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Bradykinin.
OS Lepisosteus osseus (Long-nosed gar), and
OS Awa calva (Bowfin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Semionotiformes; Lepisosteidae;
OC Lepisosteus.
OC NCBI_TaxID=34771, 7924;
RN [1]
RP SEQUENCE
RX MEDLINE=95380361; PubMed=7651903;
RA Conlon J.M.; Platzack B.; Maira J.E.; Youson J.H.; Olson K.R.;
RT "Isolation and biological activity of [Trp5]bradykinin from the plasma
RT of the phylogenetically ancient fish, the bowfin and the longnosed
RT gar."
RL Peptides 16:485-489(1995).
SQ SEQUENCE 9 AA; 1099 MW; 3393D775A3786777 CRC64;

Query Match
Best Local Similarity 33.8%; Score 24; DB 13; Length 9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGW 11
DB 3 PGW 5

RESULT 5
Q9XNR6 PRELIMINARY; PRT; 12 AA.
ID Q9XNR6;
AC Q9XNR6;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 12, Last annotation update)
DE NADH:ubiquinone oxidoreductase subunit 3 (Fragment).
GN NAD3.
OS Pyraliella littoralis.
OC Mitochondrion.
OC Eukaryota; stramenopiles; Phaeophyceae; Ectocarpales;
OC Acinetosporaceae; Pyraliella.
OC NCBI_TaxID=2885;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=roscoff;
RX MEDLINE=99346148; PubMed=10415341;
RA Oudot M.P.; Kloareg B.; Loiseaux-de Goer S.;
RT "The mitochondrial Pyraliella littoralis nad1 gene contains only the
RT N-terminal Pcs-binding domain."
RL Gene 235:131-137(1999).
DR EMBL; AF101039; AAD44051.1;
DR GO; GO:0005739; C:Mitochondrion; IEA.
KM Mitochondrion; Ubiquinone.
FT NON_TER
SQ SEQUENCE 12 AA; 1501 MW; 49750746424B5B13 CRC64;

Query Match
Best Local Similarity 33.8%; Score 24; DB 8; Length 12;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FKIKHYGP 9
DB 2 FKIKHYGP 9

RESULT 6
O12090 PRELIMINARY; PRT; 12 AA.
ID O12090;
AC O12090;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Tac Protein (Fragment).
GN TAT.

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OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCB1_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81436; AAB60826.1; -
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; I.
RN NON_TER 1
FT SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;
SQ

Query Match 33.8%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 PGM 11
DB 8 PGM 10

RESULT 7
ID 012094 PRELIMINARY; PRT; 12 AA.
AC 012094;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCB1_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81438; AAB60830.1; -
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; I.
RN NON_TER 1
FT SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;
SQ

Query Match 33.8%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 PGM 11
DB 8 PGM 10

RESULT 8
ID 012114 PRELIMINARY; PRT; 12 AA.
AC 012114;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCB1_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81436; AAB60826.1; -
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; I.
RN NON_TER 1
FT SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;
SQ

RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81448; AAB60850.1; -
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; I.
RN NON_TER 1
FT SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;
SQ

Query Match 33.8%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 PGM 11
DB 8 PGM 10

RESULT 9
ID 012082 PRELIMINARY; PRT; 12 AA.
AC 012082;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCB1_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81432; AAB60818.1; -
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; I.
RN NON_TER 1
FT SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;
SQ

Query Match 33.8%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 PGM 11
DB 8 PGM 10

RESULT 10
ID 012106 PRELIMINARY; PRT; 12 AA.
AC 012106;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCB1_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81436; AAB60826.1; -
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; I.
RN NON_TER 1
FT SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;
SQ

RT "dUpase minus CAEV is attenuated for pathogenesis and accumulates G
RT to A substitutions.";
RT Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.
DR EMBL; U81444; AAB60842.1; -
DR GO; GO:0015563; P:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; L:transcription; IEA.
DR Pfam; PF02998; L:transcription; IEA.
DR NCBI_TaxID=11660;
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;
FT NON TER 1

Query Match 33.8%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGM 11
DB 8 PGM 10

RESULT 11
ID 012092 PRELIMINARY; PRT; 12 AA.
AC 012092;
DT 01-JUL-1997 (TREMblrel. 04, Created)
DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUpase minus CAEV is attenuated for pathogenesis and accumulates G
RT to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.
DR EMBL; U81437; AAB60828.1; -
DR GO; GO:0015563; P:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; L:transcription; IEA.
DR Pfam; PF02998; L:transcription; IEA.
DR NCBI_TaxID=11660;
FT NON TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 33.8%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGM 11
DB 8 PGM 10

RESULT 12
ID 012108 PRELIMINARY; PRT; 12 AA.
AC 012108;
DT 01-JUL-1997 (TREMblrel. 04, Created)
DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUpase minus CAEV is attenuated for pathogenesis and accumulates G
RT to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.

DR EMBL; U81445; AAB60844.1; -
DR GO; GO:0015563; P:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; L:transcription; IEA.
DR Pfam; PF02998; L:transcription; IEA.
DR NCBI_TaxID=11660;
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;
FT NON TER 1

Query Match 33.8%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGM 11
DB 8 PGM 10

RESULT 13
ID 012074 PRELIMINARY; PRT; 12 AA.
AC 012074;
DT 01-JUL-1997 (TREMblrel. 04, Created)
DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUpase minus CAEV is attenuated for pathogenesis and accumulates G
RT to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.
DR EMBL; U81428; AAB60810.1; -
DR GO; GO:0015563; P:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; L:transcription; IEA.
DR Pfam; PF02998; L:transcription; IEA.
DR NCBI_TaxID=11660;
FT NON TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 33.8%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGM 11
DB 8 PGM 10

RESULT 14
ID 012116 PRELIMINARY; PRT; 12 AA.
AC 012116;
DT 01-JUL-1997 (TREMblrel. 04, Created)
DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUpase minus CAEV is attenuated for pathogenesis and accumulates G
RT to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.
DR EMBL; U81449; AAB60852.1; -
DR GO; GO:0015563; P:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.

DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; 1.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 33.8%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGM 11
DB 8 PGM 10

RESULT 15
ID 012118 PRELIMINARY; PRT; 12 AA.
AC 012118;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81450; AAB60848.1; -
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; 1.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 33.8%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGM 11
DB 8 PGM 10

RESULT 16
ID 012110 PRELIMINARY; PRT; 12 AA.
AC 012110;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81446; AAB60846.1; -
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; 1.
FT NON_TER 1

SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 33.8%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGM 11
DB 8 PGM 10

RESULT 17
ID 012112 PRELIMINARY; PRT; 12 AA.
AC 012112;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81447; AAB60848.1; -
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; 1.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 33.8%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGM 11
DB 8 PGM 10

RESULT 18
ID 012076 PRELIMINARY; PRT; 12 AA.
AC 012076;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81429; AAB60812.1; -
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; 1.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 33.8%; Score 24; DB 15; Length 12;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGM 11
Db 8 PGM 10

RESULT 19

012088 PRELIMINARY; PRT; 12 AA.
AC 012088;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dnpase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81435; AAB60824.1; -.
DR InterPro: IPR004247; Lenticviral_Tat.
DR Pfam: PF02998; Lenticviral_Tat; I.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1279 MW; 4B90BB1E8644EB7 CRC64;

Query Match 33.8%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGM 11
Db 8 PGM 10

RESULT 20

012078 PRELIMINARY; PRT; 12 AA.
AC 012078;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dnpase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81430; AAB60814.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro: IPR004247; Lenticviral_Tat.
DR Pfam: PF02998; Lenticviral_Tat; I.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BB1E8644EB7 CRC64;

Query Match 33.8%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGM 11
Db 8 PGM 10

RESULT 21

012080 PRELIMINARY; PRT; 12 AA.
AC 012080;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dnpase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81431; AAB60816.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro: IPR004247; Lenticviral_Tat.
DR Pfam: PF02998; Lenticviral_Tat; I.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BB1E8644EB7 CRC64;

Query Match 33.8%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGM 11
Db 8 PGM 10

RESULT 22

012084 PRELIMINARY; PRT; 12 AA.
AC 012084;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dnpase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81433; AAB60820.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro: IPR004247; Lenticviral_Tat.
DR Pfam: PF02998; Lenticviral_Tat; I.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BB1E8644EB7 CRC64;

Query Match 33.8%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGM 11
Db 8 PGM 10

RESULT 23

012086

ID 012086 PRELIMINARY; PRT; 12 AA.
 AC 012086;
 DT 01-JUL-1997 (TRENBLREL. 04, Created)
 DT 01-JUL-1997 (TRENBLREL. 04, Last sequence update)
 DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
 DE Tat protein (Fragment).
 GN TAT.
 OS Caprine arthritis encephalitis virus (CAEV).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OC NCBI_TaxID=11660;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Turelli P., Galigen F., Mornex J.-F., Vigne R., Querat G.;
 RT "dnpase minus CAEV is attenuated for pathogenesis and accumulates G
 RT to A substitutions."
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U81434; AAB60822.1; -
 DR GO; GO:0016563; P:transcriptional activator activity; IEA.
 DR GO; GO:0045941; P:positive regulation of transcription; IEA.
 DR InterPro; IPR004247; Lentiviral Tat.
 DR Pfam; PF02998; Lentiviral_Tat; I.
 DR NON_TER 1
 FT 1
 SQ SEQUENCE 12 AA; 1266 MW; 5A60BB1E644EB7 CRC64;

Query Match 33.8%; Score 24; DB 15; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGM 11
 Db 8 PGM 10

RESULT 24

ID 034909 PRELIMINARY; PRT; 8 AA.
 AC 034909;
 DT 01-NOV-1996 (TRENBLREL. 01, Created)
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
 DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
 DE Cytochrome b (Fragment).
 OS Locusta migratoria (Migratory locust).
 OS Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OC NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=8823478; PubMed=2836084;
 RA McCracken A., Uhlenbusch I., Gallissen G.;
 RT "Structure of the cloned Locusta migratoria mitochondrial genome:
 RT restriction mapping and sequence of its ND-1 (URF-1) gene."
 RL Curr. Genet. 11:625-630(1987).
 DR EMBL; X55286; CAA28905.1; -
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR Mitochondrion.
 KW Mitochondrion.
 FT NON_TER 1
 FT 1
 SQ SEQUENCE 8 AA; 1019 MW; F8E33723304B45B6 CRC64;

Query Match 31.0%; Score 22; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KXKH 6
 Db 5 KXKH 8

RESULT 25
 Q8MH06 PRELIMINARY; PRT; 14 AA.

AC Q8MH06;
 DT 01-OCT-2002 (TRENBLREL. 22, Created)
 DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)
 DT 01-OCT-2002 (TRENBLREL. 22, Last annotation update)
 DE MHC class II antigen (Fragment).
 GN HLA-DQA1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hoarau J.-J., Cesari M., Callens H., Cadet F., Pabion M.;
 RT "A new splicing acceptor site and polyadenylation sequence signal
 RT contribute to increase the extraordinary diversity of DQA1 mRNA
 RT isoforms."
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR [2]
 RP SEQUENCE FROM N.A.
 RA Hoarau J.-J., Cesari M., Callens H., Cadet F., Pabion M.;
 RT "HLA DQA1 gene generates multiple transcripts by alternative splicing
 RT and polyadenylation of the 3' untranslated region."
 DR EMBL; AF533934; AAM94848.1; -
 DR NON_TER 1
 FT 1
 SQ SEQUENCE 14 AA; 1435 MW; C5E8A0FE15DF8EBD CRC64;

Query Match 31.0%; Score 22; DB 7; Length 14;
 Best Local Similarity 60.0%; Pred. No. 5.5e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGP 9
 Db 9 RHQGP 13

RESULT 26

ID Q8MH35 PRELIMINARY; PRT; 14 AA.
 AC Q8MH35;
 DT 01-OCT-2002 (TRENBLREL. 22, Created)
 DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)
 DT 01-OCT-2002 (TRENBLREL. 22, Last annotation update)
 DE MHC class II antigen (Fragment).
 GN HLA-DQA1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hoarau J.-J., Cesari M., Callens H., Cadet F., Pabion M.;
 RT "A new splicing acceptor site and polyadenylation sequence signal
 RT contribute to increase the extraordinary diversity of DQA1 mRNA
 RT isoforms."
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR [2]
 RP SEQUENCE FROM N.A.
 RA Hoarau J.-J., Cesari M., Callens H., Cadet F., Pabion M.;
 RT "HLA DQA1 gene generates multiple transcripts by alternative splicing
 RT and polyadenylation of the 3' untranslated region."
 DR EMBL; AF533905; AAM94819.1; -
 DR NON_TER 1
 FT 1
 SQ SEQUENCE 14 AA; 1435 MW; C5E8A0FE15DF8EBD CRC64;

Query Match 31.0%; Score 22; DB 7; Length 14;
 Best Local Similarity 60.0%; Pred. No. 5.5e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGP 9
 Db 9 RHQGP 13

RESULT 27

Q8MH39

ID Q8MH39

PRELIMINARY; PRT; 14 AA.

AC Q8MH39; 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE MHC class II antigen (Fragment).

GN HLA-DQA1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Hoarau J.-J., Cesari M., Callens H., Cadet F., Pabion M.;

RT "A new splicing acceptor site and polyadenylation sequence signal

RT contribute to increase the extraordinary diversity of DQA1 mRNA

RT isoforms."

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Hoarau J.-J., Cesari M., Callens H., Cadet F., Pabion M.;

RT "HLA DQA1 gene generates multiple transcripts by alternative splicing

RT and polyadenylation of the 3' untranslated region."

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF533901; AAM94815.1; -

DR NCBI_TaxID=9606;

FT NON TER

SQ SEQUENCE 14 AA; 1435 MW; CSEEAOFELSDP8EBD CRC64;

Query Match

Best Local Similarity 31.0%; Score 22; DB 7; Length 14;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KHYGP 9

Db 9 RHQGP 13

RESULT 28

Q8MH18

ID Q8MH18

PRELIMINARY; PRT; 14 AA.

AC Q8MH18; 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE MHC class II antigen (Fragment).

GN HLA-DQA1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Hoarau J.-J., Cesari M., Callens H., Cadet F., Pabion M.;

RT "A new splicing acceptor site and polyadenylation sequence signal

RT contribute to increase the extraordinary diversity of DQA1 mRNA

RT isoforms."

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Hoarau J.-J., Cesari M., Callens H., Cadet F., Pabion M.;

RT "HLA DQA1 gene generates multiple transcripts by alternative splicing

RT and polyadenylation of the 3' untranslated region."

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF533922; AAM94836.1; -

DR NCBI_TaxID=9606;

FT NON TER

SQ SEQUENCE 14 AA; 1435 MW; CSEEAOFELSDP8EBD CRC64;

Query Match

Best Local Similarity 31.0%; Score 22; DB 7; Length 14;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KHYGP 9

Db 9 RHQGP 13

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 29

Q8MH55

ID Q8MH55

PRELIMINARY; PRT; 14 AA.

AC Q8MH55; 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE MHC class II antigen (Fragment).

GN HLA-DQA1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Hoarau J.-J., Cesari M., Callens H., Cadet F., Pabion M.;

RT "HLA-DQA1 gene generate multiple transcripts by alternative splicing

RT and polyadenylation of the 3' UTR."

RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF15808; AAM74915.1; -

DR NCBI_TaxID=9606;

FT NON TER

SQ SEQUENCE 14 AA; 1435 MW; CSEEAOFELSDP8EBD CRC64;

Query Match

Best Local Similarity 31.0%; Score 22; DB 7; Length 14;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KHYGP 9

Db 9 RHQGP 13

RESULT 30

Q8MH40

ID Q8MH40

PRELIMINARY; PRT; 14 AA.

AC Q8MH40; 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE MHC class II antigen (Fragment).

GN HLA-DQA1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Hoarau J.-J., Cesari M., Callens H., Cadet F., Pabion M.;

RT "A new splicing acceptor site and polyadenylation sequence signal

RT contribute to increase the extraordinary diversity of DQA1 mRNA

RT isoforms."

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Hoarau J.-J., Cesari M., Callens H., Cadet F., Pabion M.;

RT "HLA DQA1 gene generates multiple transcripts by alternative splicing

RT and polyadenylation of the 3' untranslated region."

RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF533900; AAM94814.1; -

DR NCBI_TaxID=9606;

FT NON TER

SQ SEQUENCE 14 AA; 1435 MW; CSEEAOFELSDP8EBD CRC64;

Query Match

Best Local Similarity 31.0%; Score 22; DB 7; Length 14;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KHYGP 9

Db 9 RHQGP 13

QY 5 KHVGP 9
: |||
Db 9 RHQGP 13

RESULT 31

Q8MH07 PRELIMINARY; PRT; 14 AA.
AC Q8MH07:
DT 01-OCT-2002 (TRENBLREL. 22, Created)
DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)
DT 01-OCT-2002 (TRENBLREL. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQA1 mRNA
RT isoforms."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
[2]
RN [2]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "HLA-DQA1 gene generates multiple transcripts by alternative splicing
RT and polyadenylation of the 3' untranslated region."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF533933; AAM94847.1; -.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1435 MW; CSEBA0FE15DF8EBD CRC64;

Query Match 31.0%; Score 22; DB 7; Length 14;
Best Local Similarity 60.0%; Pred. No. 5.5e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHVGP 9
: |||
Db 9 RHQGP 13

RESULT 32

Q8MH04 PRELIMINARY; PRT; 14 AA.
AC Q8MH04:
DT 01-OCT-2002 (TRENBLREL. 22, Created)
DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)
DT 01-OCT-2002 (TRENBLREL. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQA1 mRNA
RT isoforms."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
[2]
RN [2]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "HLA-DQA1 gene generates multiple transcripts by alternative splicing
RT and polyadenylation of the 3' untranslated region."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF533936; AAM94850.1; -.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1435 MW; CSEBA0FE15DF8EBD CRC64;

Query Match 31.0%; Score 22; DB 7; Length 14;
Best Local Similarity 60.0%; Pred. No. 5.5e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHVGP 9
: |||
Db 9 RHQGP 13

RESULT 33

Q8MH52 PRELIMINARY; PRT; 14 AA.
AC Q8MH52:
DT 01-OCT-2002 (TRENBLREL. 22, Created)
DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)
DT 01-OCT-2002 (TRENBLREL. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "HLA-DQA1 genes generate multiple transcripts by alternative splicing
RT and polyadenylation of the 3' UTR."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF515811; AAM74918.1; -.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1435 MW; CSEBA0FE15DF8EBD CRC64;

Query Match 31.0%; Score 22; DB 7; Length 14;
Best Local Similarity 60.0%; Pred. No. 5.5e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHVGP 9
: |||
Db 9 RHQGP 13

RESULT 34

Q8MH26 PRELIMINARY; PRT; 14 AA.
AC Q8MH26:
DT 01-OCT-2002 (TRENBLREL. 22, Created)
DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)
DT 01-OCT-2002 (TRENBLREL. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQA1 mRNA
RT isoforms."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
[2]
RN [2]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "HLA-DQA1 gene generates multiple transcripts by alternative splicing
RT and polyadenylation of the 3' untranslated region."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF533914; AAM94828.1; -.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1435 MW; CSEBA0FE15DF8EBD CRC64;

Query Match 31.0%; Score 22; DB 7; Length 14;

Best Local Similarity 60.0%; Pred. No. 5.5e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGP 9
: |||
Db 9 RHQGP 13

RESULT 35

ID Q8MH53 PRELIMINARY; PRT; 14 AA.
AC Q8MH53;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "HLA-DQA1 gene generates multiple transcripts by alternative splicing
RT and polyadenylation of the 3' UTR.";
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF515810; AAM74917.1; -.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1435 MW; CSEEA0FE15DF8EBD CRC64;

Query Match 31.0%; Score 22; DB 7; Length 14;
Best Local Similarity 60.0%; Pred. No. 5.5e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGP 9
: |||
Db 9 RHQGP 13

RESULT 36

ID Q8MH20 PRELIMINARY; PRT; 14 AA.
AC Q8MH20;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQA1 mRNA
RT isoforms.";
RL Submitted (Jul-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "HLA DQA1 gene generates multiple transcripts by alternative splicing
RT and polyadenylation of the 3' untranslated region.";
RL Submitted (Jul-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF533920; AAM94834.1; -.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1435 MW; CSEEA0FE15DF8EBD CRC64;

Query Match 31.0%; Score 22; DB 7; Length 14;
Best Local Similarity 60.0%; Pred. No. 5.5e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGP 9
: |||
Db 9 RHQGP 13

RESULT 37

ID Q8MH27 PRELIMINARY; PRT; 14 AA.
AC Q8MH27;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQA1 mRNA
RT isoforms.";
RL Submitted (Jul-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "HLA DQA1 gene generates multiple transcripts by alternative splicing
RT and polyadenylation of the 3' untranslated region.";
RL Submitted (Jul-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF533913; AAM94827.1; -.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1435 MW; CSEEA0FE15DF8EBD CRC64;

Query Match 31.0%; Score 22; DB 7; Length 14;
Best Local Similarity 60.0%; Pred. No. 5.5e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGP 9
: |||
Db 9 RHQGP 13

RESULT 38

ID Q8MH05 PRELIMINARY; PRT; 14 AA.
AC Q8MH05;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQA1 mRNA
RT isoforms.";
RL Submitted (Jul-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "HLA DQA1 gene generates multiple transcripts by alternative splicing
RT and polyadenylation of the 3' untranslated region.";
RL Submitted (Jul-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF533935; AAM94849.1; -.
FT NON_TER 1 1

SQ SEQUENCE 14 AA; 1435 MW; CSEBAOFE15DF8EBD CRC64;
 Query Match 31.0%; Score 22; DB 7; Length 14;
 Best Local Similarity 60.0%; Pred. No. 5.5e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHVGP 9
 : |||
 Db 9 RHQGP 13

RESULT 39
 Q8MH16 PRELIMINARY; PRT; 14 AA.
 AC Q8MH16;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE MHC class II antigen (Fragment).
 GN HLA-DQA1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
 RT "A new splicing acceptor site and polyadenylation sequence signal
 RT contribute to increase the extraordinary diversity of DQA1 mRNA
 RT isoforms.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF533924; AAM94838.1; -.
 FT NON_TER
 SQ SEQUENCE 14 AA; 1435 MW; CSEBAOFE15DF8EBD CRC64;

Query Match 31.0%; Score 22; DB 7; Length 14;
 Best Local Similarity 60.0%; Pred. No. 5.5e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHVGP 9
 : |||
 Db 9 RHQGP 13

RESULT 40
 Q8MH38 PRELIMINARY; PRT; 14 AA.
 AC Q8MH38;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE MHC class II antigen (Fragment).
 GN HLA-DQA1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
 RT "A new splicing acceptor site and polyadenylation sequence
 RT contribute to increase the extraordinary diversity of DQA1 mRNA
 RT isoforms.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF533924; AAM94838.1; -.
 FT NON_TER
 SQ SEQUENCE FROM N.A.
 RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;

RT "HLA DQA1 gene generates multiple transcripts by alternative splicing
 RT and polyadenylation of the 3' untranslated region.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF533902; AAM94816.1; -.
 FT NON_TER
 SQ SEQUENCE 14 AA; 1435 MW; CSEBAOFE15DF8EBD CRC64;

Query Match 31.0%; Score 22; DB 7; Length 14;
 Best Local Similarity 60.0%; Pred. No. 5.5e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHVGP 9
 : |||
 Db 9 RHQGP 13

RESULT 41
 Q8MH56 PRELIMINARY; PRT; 14 AA.
 AC Q8MH56;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE MHC class II antigen (Fragment).
 GN HLA-DQA1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
 RT "HLA-DQA1 genes generate multiple transcripts by alternative splicing
 RT and polyadenylation of the 3' UTR.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF515807; AAM74914.1; -.
 FT NON_TER
 SQ SEQUENCE 14 AA; 1435 MW; CSEBAOFE15DF8EBD CRC64;

Query Match 31.0%; Score 22; DB 7; Length 14;
 Best Local Similarity 60.0%; Pred. No. 5.5e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHVGP 9
 : |||
 Db 9 RHQGP 13

RESULT 42
 Q8MH14 PRELIMINARY; PRT; 14 AA.
 AC Q8MH14;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE MHC class II antigen (Fragment).
 GN HLA-DQA1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
 RT "A new splicing acceptor site and polyadenylation sequence signal
 RT contribute to increase the extraordinary diversity of DQA1 mRNA
 RT isoforms.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF515807; AAM74914.1; -.
 FT NON_TER
 SQ SEQUENCE FROM N.A.
 RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
 RT "HLA DQA1 gene generates multiple transcripts by alternative splicing
 RT and polyadenylation of the 3' untranslated region.";

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF533926; AAM94840.1; -
 FT NON_TER 1
 SQ SEQUENCE 14 AA; 1435 MW; CSEBA0FB15DF8EBD CRC64;
 Query Match 31.0%; Score 22; DB 7; Length 14;
 Best Local Similarity 60.0%; Pred. No. 5.5e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGP 9
 :|||
 Db 9 RHQGP 13

RESULT 43
 Q8MH31 PRELIMINARY; PRT; 14 AA.
 AC Q8MH31;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE MHC class II antigen (Fragment).
 GN HLA-DQA1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hoarau J.-J., Cesari M., Calliens H., Cadet F., Pablon M.;
 RT "A new splicing acceptor site and polyadenylation sequence signal
 RT contribute to increase the extraordinary diversity of DQA1 mRNA
 RT isoforms.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Hoarau J.-J., Cesari M., Calliens H., Cadet F., Pablon M.;
 RT "HLA DQA1 gene generates multiple transcripts by alternative splicing
 RT and polyadenylation of the 3' untranslated region.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF533909; AAM94823.1; -
 FT NON_TER 1
 SQ SEQUENCE 14 AA; 1435 MW; CSEBA0FB15DF8EBD CRC64;
 Query Match 31.0%; Score 22; DB 7; Length 14;
 Best Local Similarity 60.0%; Pred. No. 5.5e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGP 9
 :|||
 Db 9 RHQGP 13

RESULT 44
 Q8MH30 PRELIMINARY; PRT; 14 AA.
 AC Q8MH30;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE MHC class II antigen (Fragment).
 GN HLA-DQA1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hoarau J.-J., Cesari M., Calliens H., Cadet F., Pablon M.;
 RT "A new splicing acceptor site and polyadenylation sequence signal
 RT contribute to increase the extraordinary diversity of DQA1 mRNA
 RT isoforms.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

RN [2]
 RP SEQUENCE FROM N.A.
 RA Hoarau J.-J., Cesari M., Calliens H., Cadet F., Pablon M.;
 RT "HLA DQA1 gene generates multiple transcripts by alternative splicing
 RT and polyadenylation of the 3' untranslated region.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF533910; AAM94824.1; -
 FT NON_TER 1
 SQ SEQUENCE 14 AA; 1435 MW; CSEBA0FB15DF8EBD CRC64;
 Query Match 31.0%; Score 22; DB 7; Length 14;
 Best Local Similarity 60.0%; Pred. No. 5.5e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGP 9
 :|||
 Db 9 RHQGP 13

RESULT 45
 Q8MH51 PRELIMINARY; PRT; 14 AA.
 AC Q8MH51;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE MHC class II antigen (Fragment).
 GN HLA-DQA1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hoarau J.-J., Cesari M., Calliens H., Cadet F., Pablon M.;
 RT "HLA-DQA1 genes generate multiple transcripts by alternative splicing
 RT and polyadenylation of the 3' UTR.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF515812; AAM74919.1; -
 FT NON_TER 1
 SQ SEQUENCE 14 AA; 1435 MW; CSEBA0FB15DF8EBD CRC64;
 Query Match 31.0%; Score 22; DB 7; Length 14;
 Best Local Similarity 60.0%; Pred. No. 5.5e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGP 9
 :|||
 Db 9 RHQGP 13

Search completed: August 30, 2004, 10:55:21
 Job time : 13.5912 secs

Thu Sep 2 07:41:39 2004

us-09-720-469a-5.aug30.rsp

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:09 ; Search time 1.89527 Seconds
(without alignments)
302.211 Million cell updates/sec

Title: US-09-720-469A-5

Perfect score: 71

Sequence: 1 NFKLKHGPGW 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 585

Minimum DB seq length: 8

Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	29	40.8	11 1 CA31_LITCI	P82089 litorea cit
2	29	40.8	11 1 CA32_LITCI	P82090 litorea cit
3	28	39.4	8 1 RPCH_PANBO	P08339 pandanus bo
4	28	39.4	10 1 HTF_NAUCI	P10939 nauphoeta c
5	26	36.6	10 1 GON2_CHICK	P37043 gallus gall
6	26	36.6	10 1 GON1_SQUAC	P27425 squallus aca
7	25	35.2	8 1 AKH_MEML	P25423 meiolanthe
8	25	35.2	8 1 AKH_TROBAT	P14595 tabanus atr
9	25	35.2	10 1 GON3_ONCKE	P20367 oncorhynch
10	25	35.2	10 1 HTF_TABAT	P14596 tabanus atr
11	24	33.8	10 1 BRK_ONCMY	O98221 oncorhynch
12	24	33.4	10 1 COXO_RAT	P80432 rattus norv
13	23	32.4	10 1 COXO_TROUB	P80982 thunnus obe
14	22	31.0	8 1 HTF_PPRAM	P04548 periplaneta
15	22	31.0	8 1 HTF_TENMO	P25419 tenebrio mo
16	22	31.0	10 1 GON1_PETMA	P04378 petromyzon
17	22	31.0	10 1 COR2_PPRAM	P11496 periplaneta
18	22	31.0	13 1 BOML_PSEGU	P42991 pseudophryn
19	20	28.2	8 1 AKHG_GRYBI	P14086 gryllus bim
20	20	28.2	8 1 AKH_TIRAU	P25418 libellula a
21	20	28.2	10 1 HTP1_ROMMI	P18110 romalea mic
22	20	28.2	10 1 NUDM_CANFA	P54713 canis fami
23	19.5	27.5	12 1 RFI_CONSP	P58805 conus spuri
24	19	26.8	8 1 HTF2_PPRAM	P04549 periplaneta
25	19	26.8	10 1 GON3_PETMA	P30348 petromyzon
26	19	26.8	10 1 HTP2_CARMO	P11385 carausius m
27	19	26.8	10 1 HTP_HERZE	P16535 heliothis z
28	18	25.4	11 1 CSIE_BACSU	P81095 bacillus su
29	18	25.4	13 1 MIA_CANDR	P01198 camelus dro
30	18	25.4	13 1 SA2B_ONCMY	P82238 oncorhynch
31	18	25.4	13 1 SA2B_ONCMY	P82239 oncorhynch
32	18	25.4	13 1 UN12_CLOPA	P81353 clostridium
33	18	25.4	14 1 LPW_ECOLI	P03053 escherichia

34	18	25.4	14 1 MCR2_METTM	P58816 methanobact
35	17	23.9	8 1 AL1A_CYDPO	P82152 cydia pomon
36	17	23.9	8 1 CCRN_MACEU	P30369 macropus eu
37	17	23.9	1 1 UF06_MOUSE	P38644 mus musculu
38	17	23.9	9 1 LIMP_LOCOMI	P31799 locusta mig
39	17	23.9	10 1 BPP_VIPAS	P31351 vipera aspi
40	17	23.9	10 1 CA12_LITCI	P82086 litorea cit
41	17	23.9	10 1 CAER_LITXA	P56284 litorea xan
42	17	23.9	10 1 TKN1_SCYCA	P08608 scyllorhinu
43	17	23.9	10 1 TK51_AEDAE	P42634 aedes aegypt
44	17	23.9	10 1 TK52_AEDAE	P42635 aedes aegypt
45	17	23.9	10 1 UXA6_CHLTR	P38007 chlamydia t

ALIGNMENTS

CA31_LITCI	STANDARD;	PRT;	11 AA.
AC	P82089;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Caerulein 3.1/3.1y4.		
OS	Litorea citropa (Australian blue mountains tree frog).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;		
OC	Pelodytidae; Litorea.		
OX	NCB1_TaxID=94770;		
RM	[1]		
RP	SEQUENCE AND MASS SPECTROMETRY.		
RC	TISSUE=Skin secretion;		
KX	MEDLINE=20057701; PubMed=10589099;		
FA	Wadnitz P.A.; Bowie U.H.; Tyler M.U.;		
RT	"Caerulein-like peptides from the skin glands of the Australian blue mountains tree frog Litorea citropa. Part 1. Sequence determination using electrospray mass spectrometry."		
RT	using electrospray mass spectrometry."		
RL	Rapid Commun. Mass Spectrom. 13:2498-2502(1999).		
CC	-1- FUNCTION: Hypotensive neuropeptide (Probable).		
CC	-1- SUBCELLULAR LOCATION: Secreted.		
CC	-1- TISSUE SPECIFICITY: Skin dorsal glands.		
CC	-1- PTM: Isoform 3.1y4 differs from isoform 3.1 in not being sulfated.		
CC	-1- MASS SPECTROMETRY: MW=1407; METHOD=Electrospray.		
CC	-1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.		
DR	InterPro: IPR001651; Gastrin.		
DR	PROSITE: PS00259; GASTRIN; FALSE_NEG.		
KW	Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;		
FT	MOD_RES 1 4 PYROGLUTAMINE CARBOXYLIC ACID.		
FT	MOD_RES 4 4 SULFATION.		
FT	MOD_RES 11 11 AMIDATION.		
SEQ	SEQUENCE 11 AA, 1347 MW, 100DAB7676618A86B CRC64;		
QY	7 YGPGM 11		
DB	4 YGTGW 8		
Query Match	40.8%; Score 29; DB 1; Length 11;		
Best Local Similarity	80.0%; Pred. No. 34;		
Matches	4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
RESULT 2			
CA32_LITCI	STANDARD;	PRT;	11 AA.
AC	P82090;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Caerulein 3.2/3.2y4.		
OS	Litorea citropa (Australian blue mountains tree frog).		

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulins-like peptides from the skin glands of the Australian blue
RT mounting tree frog Litoria citropa. Part 1. Sequence determination
RT using electrospray mass spectrometry";
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
CC -1- FUNCTION: Hypotensive neuropeptide (Probable).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin dorsal glands.
CC -1- PTM: Isoform 3.2Y4 differs from isoform 3.2 in not being
CC sulfated.
CC -1- MASS SPECTROMETRY: MW=1423; METHOD=Electrospray.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro: IPR001651; Gastrin.
DR PROSITE: PS00259; GASTRIN; FALSE NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyroglutamate carboxylic acid.
FT MOD RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.
FT MOD RES 4 4 SULFATION.
FT MOD RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1363 MW; 10DAB8867861A86B CRC64;
Query Match 40.8%; Score 29; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 34;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 7 YGPGW 11
DB 4 YGTGW 8
RESULT 3
ID RPCH_PANBO STANDARD; PRT; 8 AA.
AC P08939;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Red pigment concentrating hormone (RPCH).
OS Pandanus borealis (Northern red shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea; Pandalioidea;
OC Pandalidae; Pandalus.
OX NCBI_TaxID=6703;
RN [1]
RP SEQUENCE.
RX MEDLINE=75054965; PubMed=4433569;
RA Fernlund P.;
RT "Structure of the red-pigment-concentrating hormone of the shrimp,
RT Pandanus borealis.";
RL Biochim. Biophys. Acta 371:304-311(1974).
CC -1- FUNCTION: This hormone adapts the animal to light backgrounds by
CC stimulating concentration of the pigment of its red body-
CC chromatophores.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.
DR PIR: A61348; A61348.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Pigment; Hormone; Amidation; Pyroglutamate carboxylic acid.
FT MOD RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 948 MW; 86786775B9C44736 CRC64;
Query Match 39.4%; Score 28; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 14e+05;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 6 HYGPW 11
DB 3 NFGPW 8
RESULT 4
ID HTP_NAUCI STANDARD; PRT; 10 AA.
AC P10939;
DT 01-JUN-1989 (Rel. 11, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrehalosemic hormone (HTH) (Hypertrehalosemic neuropeptide).
OS Nauphaea cinerea (Cinereous cockroach) (Gray cockroach).
OS Leucophaea maderae (Madeira cockroach).
OS Blattella germanica (German cockroach), and
OS Gryllotalpa orientalis (Madagascan hissing cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Nauphaea; Nauphaea.
OX NCBI_TaxID=6990, 6988, 6973, 36953;
RN [1]
RP SEQUENCE.
RC SPECIES=N. cinerea; TISSUE=Corpora cardiaca;
RX MEDLINE=87100208; PubMed=3801028;
RA Gaede G., Rinehart K.L., Jr.;
RT "Amino acid sequence of a hypertrehalosemic neuropeptide from the
RT corpus cardiaca of the cockroach, Nauphaea cinerea.";
RL Biochem. Biophys. Res. Commun. 141:774-781(1986).
RN [2]
RP SEQUENCE.
RC SPECIES=L. maderae, G. portentosa, and B. germanica;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L., Jr.;
RT "Primary structures of hypertrehalosemic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Gryllotalpa orientalis, Blattella germanica, and Blatta orientalis
RT and of the stick insect Ectophasma tigratum assigned by tandem fast
RT atom bombardment mass spectrometry";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
RN [3]
RP SEQUENCE.
RC SPECIES=B. germanica;
RX MEDLINE=91179584; PubMed=2080017;
RA Venera J.A., Camps F.;
RT "Structure of the hypertrehalosemic neuropeptide of the German
RT cockroach, Blattella germanica.";
RL Neuropeptides 15:107-109(1990).
CC -1- FUNCTION: Hypertrehalosemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph (trehalose is the
CC major carbohydrate in the hemolymph of insects).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.
DR PIR: A26181; A26181.
DR PIR: A60421; A60421.
DR PIR: S08997; S08997.
DR PIR: S08998; S08998.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyroglutamate carboxylic acid.
FT MOD RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.
FT MOD RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1092 MW; 056236786775B9C4 CRC64;
Query Match 39.4%; Score 28; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 47;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 6 HYGPW 11
DB 3 NFGPW 8

RESULT 5

GON2_CHICK STANDARD; PRT; 10 AA.

ID GON2_CHICK PRT; 10 AA.

AC P37043; P20408; P81750;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Gonadotropin II (Gonadotropin-releasing hormone II) (GNRH-II)

DE (LH-RH II) (Luliberin II).

OS Gallus gallus (Chicken).

OS Alligator mississippiensis (American alligator).

OS Squallus acanthias (Spiny dogfish).

OS Hydrolagus colliei (Spotted ratfish) (Pacific ratfish), and

OS Clupea pallasii (Pacific herring).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031, 8496, 7797, 7873, 30724;

RN [1]

RP SEQUENCE.

RC SPECIES=Chicken; TISSUE=Hypothalamus;

RX MEDLINE=84222059; PubMed=6427779;

RA Miyamoto K., Hasegawa Y., Nomura M., Igarashi M., Kangawa K.,

RA Matsuo H.;

RT "Identification of the second gonadotropin-releasing hormone in

RT chicken hypothalamus: evidence that gonadotropin secretion is

RT probably controlled by two distinct gonadotropin-releasing hormones

RT in avian species.";

RT Proc. Natl. Acad. Sci. U.S.A. 81:3874-3878 (1984).

RN [2]

RP SEQUENCE.

RC SPECIES=A. mississippiensis; TISSUE=Brain;

RX MEDLINE=91352338; PubMed=1682082;

RA Lovejoy D.A., Fischer W.H., Ngamwongchon S., Craig A.G.,

RA Lane V., Swanson P., Rivier J.E., Sherwood N.M.;

RT "Primary structure of two forms of gonadotropin-releasing hormone

RT from brains of the American alligator (Alligator mississippiensis).";

RT Regul. Pept. 33:105-116 (1991).

RN [3]

RP SEQUENCE.

RC SPECIES=S. acanthias; TISSUE=Brain;

RX MEDLINE=92335300; PubMed=1631133;

RA Lovejoy D.A., Fischer W.H., Ngamwongchon S., Craig A.G.,

RA Nahornik C.S., Peter R.E., Rivier J.E., Sherwood N.M.;

RT "Distinct sequence of gonadotropin-releasing hormone (GNRH) in

RT dogfish brain provides insight into GNRH evolution.";

RT Proc. Natl. Acad. Sci. U.S.A. 89:6373-6377 (1992).

RN [4]

RP SEQUENCE.

RC SPECIES=H. colliei; TISSUE=Brain;

RX MEDLINE=91340067; PubMed=1678723;

RA Lovejoy D.A., Sherwood N.M., Fischer W.H., Jackson B.C., Rivier J.E.,

RA Lee T.;

RT "Primary structure of gonadotropin-releasing hormone from the brain

RT of a holoccephalan (ratfish: Hydrolagus colliei).";

RT Gen. Comp. Endocrinol. 82:152-161 (1991).

RN [5]

RP SEQUENCE, AND FUNCTION.

RC SPECIES=C. pallasi; TISSUE=Brain, and Pituitary;

RX MEDLINE=20114331; PubMed=10650929;

RA Carolefeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,

RA Chang J.P., Rivier J.E., Sherwood N.M.;

RT "Primary structure and function of three gonadotropin-releasing

RT hormones, including a novel form, from an ancient teleost, herring.";

RT Endocrinology 141:505-512 (2000).

CC -1- FUNCTION: Stimulates the secretion of gonadotropins.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the GNRH family.

CC PIR; A61126; A61126.

DR PIR; B46030; B46030.

DR PIR; B60066; B60066.

DR InterPro: IPR002012; GNRH.

DR Pfam: PF00446; GNRH; 1.

DR PROSITE: PS00473; GNRH; 1.

KW Hormone; Amidation; Hypothalamus; Pyroglutamate carboxylic acid.

FT MOD_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.

FT MOD_RES 10 10 AMIDATION.

SQ SEQUENCE 10 AA; 1254 MW; 284B2E437871F5A3 CRC64;

Query Match

Best Local Similarity 42.9%; Score 26; DB 1; Length 10;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 KHYGPGW 11

Db 1 QHWSHGW 7

RESULT 6

GONL_SQUAC STANDARD; PRT; 10 AA.

ID GONL_SQUAC PRT; 10 AA.

AC P27429;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Gonadotropin (Gonadotropin-releasing hormone) (GNRH) (LH-RH)

DE (Luliberin).

OS Squallus acanthias (Spiny dogfish).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;

OC Elasmobranchii; Squalae; Squaloidei; Squalidae; Squalus.

OX NCBI_TaxID=7797;

RN [1]

RP SEQUENCE.

RC TISSUE=Brain;

RX MEDLINE=92335300; PubMed=1631133;

RA Lovejoy D.A., Fischer W.H., Ngamwongchon S., Craig A.G.,

RA Nahornik C.S., Peter R.E., Rivier J.E., Sherwood N.M.;

RT "Distinct sequence of gonadotropin-releasing hormone (GNRH) in

RT dogfish brain provides insight into GNRH evolution.";

RT Proc. Natl. Acad. Sci. U.S.A. 89:6373-6377 (1992).

CC -1- FUNCTION: Stimulates the secretion of gonadotropins.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the GNRH family.

CC PIR; A46030; A46030.

DR InterPro: IPR002012; GNRH.

DR Pfam; PF00446; GNRH; 1.

DR PROSITE; PS00473; GNRH; 1.

KW Hormone; Amidation; Hypothalamus; Pyroglutamate carboxylic acid.

FT MOD_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.

FT MOD_RES 10 10 AMIDATION.

SQ SEQUENCE 10 AA; 1204 MW; 284B32337871F5A3 CRC64;

Query Match

Best Local Similarity 42.9%; Score 26; DB 1; Length 10;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 KHYGPGW 11

Db 1 QHWSHGW 7

RESULT 7

AGH_MEIML STANDARD; PRT; 8 AA.

ID AGH_MEIML PRT; 8 AA.

AC P25423;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Adipokine hormone (AKH).

OS Melolontha melolontha (Cockchafer).

OS Geophilus stercorarius (Dor beetle), and

OC Pachnoda marginata (Flower beetle).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygora;

OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Scarabaeiformia;

CC Scarabaeidae; Melolonthinae; Melolontha.
 OX NCBI_TaxID=7061, 7087, 7058;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Melolontha, and G.stercorosus; TISSUE=Corpora cardiaca;
 RX MEDLINE=91248100; PubMed=2039445;
 RA Gaede G.;
 RT "A unique charged tyrosine-containing member of the adipokinetic hormone/red-pigment-concentrating hormone peptide family isolated and RT sequenced from two beetle species.";
 RL Biochem. J. 275:671-677(1991).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=P.marginata; TISSUE=Corpora cardiaca;
 RX MEDLINE=92265187; PubMed=1586453;
 RA Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;
 RT "Primary structures of neuropeptides isolated from the corpora RT cardiaca of various cetonid beetle species determined by RT pulsed-liquid phase sequencing and tandem fast atom bombardment mass spectrometry";
 RL Biol. Chem. Hoppe-Seyler 373:133-142(1992).
 CC -1- FUNCTION: This hormone, released from cells in the corpora CC cardiaca after the beginning of flight, causes release of CC diglycerides from the fat body and then stimulates the flight CC muscles to use these diglycerides as an energy source.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.
 CC PIR: A58641; A58641.
 DR PIR: A58641; A58641.
 DR PIR: S15422; S15422.
 DR PIR: S21663; S21663.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 DR Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 1022 MW; 867AB775AB544736 CRC64;
 QY 6 HXPGW 11
 Db 3 NVSPDW 8
 Query Match 35.2%; Score 25; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 8
 AKH_TABAT STANDARD; PRT; 8 AA.
 ID AKH_TABAT
 AC P14595;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I) (DCC 1).
 OS Tabanus atratus (Horse fly).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
 CC Tabanus.
 OX NCBI_TaxID=7207;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=90046758; PubMed=2813385;
 RA Jaffe H., Rahna A.K., Riley C.T., Fraser B.A., Nachman R.J.,
 RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
 RT "Primary structure of two neuropeptide hormones with adipokinetic and RT hypotrehalosemic activity isolated from the corpora cardiaca of horse RT flies (Diptera)";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
 CC -1- FUNCTION: This hormone, released from cells in the corpora CC cardiaca after the beginning of flight, causes release of CC diglycerides from the fat body and then stimulates the flight

CC muscles to use these diglycerides as an energy source.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.
 CC PIR: A33995; A33995.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 DR Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;
 QY 7 YXPGW 11
 Db 4 FTPGW 8
 Query Match 35.2%; Score 25; DB 1; Length 8;
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 9
 GON3_ONCKE STANDARD; PRT; 10 AA.
 ID GON3_ONCKE
 AC P20367; B81751.
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gonadoliberin III (Gonadotropin-releasing hormone III) (GNRH-III) (LH- RH III) (Lutiberin III).
 GN GNRH3.
 OS Oncorhynchus keta (Chum salmon), and
 OS Clupea pallasii (Pacific herring).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 CC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8018, 30724;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=O.keta;
 RX MEDLINE=83195140; PubMed=6341999;
 RA Sherwood N., Eiden L., Brownstein M., Spiess J., Rivier J., Vale W.;
 RT "Characterization of a teleost gonadotropin-releasing hormone.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:2794-2798(1983).
 RN [2]
 RP SEQUENCE AND FUNCTION.
 RC SPECIES=C.pallasii; TISSUE=Brain, and Pituitary;
 RX MEDLINE=20114351; PubMed=10650929;
 RA Carlsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,
 RA Chang J.P., Rivier J.E., Sherwood N.M.;
 RT "Primary structure and function of three gonadotropin-releasing RT hormones, including a novel form, from an ancient teleost, herring.";
 RL Endocrinology 141:505-512(2000).
 CC -1- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates CC the secretion of both luteinizing and follicle-stimulating CC hormones.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the GnRH family.
 CC PIR: A21114; A21114.
 DR InterPro: IPR002012; GNRH.
 DR Pfam: PF00446; GNRH; 1.
 DR PROSITE: PS00473; GNRH; 1.
 DR Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1230 MW; 284B233786B4543 CRC64;
 QY 5 HXPGW 11
 Db 1 QHWSTGW 7
 Query Match 35.2%; Score 25; DB 1; Length 10;
 Best Local Similarity 42.9%; Pred. No. 1.6e+02;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;


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RESULT 10
HTF TABAT
ID HTF TABAT STANDARD; PRT; 10 AA.
AC P14596;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrihaloasemic factor (HOTH) (Dipteran corpora cardiaca factor II)
DE (DCC II).
OS Tabanus atratus (Horse fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
OC Tabanus.
OX NCBI_TaxID=7207;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RC MEDLINE=90046758; PubMed=2813385;
RX Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RX Vogel V.W., Zhang Y.-S., Hayes D.K.;
RA "Primary structure of two neuropeptide hormones with adipokinetic and
RA hypertrihaloasemic activity isolated from the corpora cardiaca of horse
RA flies (Diptera)".
RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC -1- FUNCTION: Hypertrihaloasemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph of insects.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPOG family.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD RES 1 10 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1169 MW; 916036786771A9D1 CRC64;

Query Match 35.2%; Score 25; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 YGPGW 11
: |||
Db 4 FTFGW 8

RESULT 11
BRK ONCMY
ID BRK ONCMY STANDARD; PRT; 10 AA.
AC 09PR1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lysyl-bradykinin-like.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Proteanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RX MEDLINE=94039817; PubMed=8224232;
RA Conlon J.M., Olson K.R.;
RT "Purification of a vasoactive peptide related to lysyl-bradykinin from
RT trout plasma".
RL FEBS Lett. 334:175-78(1993).
CC -1- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR
CC THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Plasma.
CC -1- SIMILARITY: Belongs to the bradykinin family.

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DR PIR; S39030; S39030.
KW Bradykinin; Vasodilator.
SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;

Query Match 33.8%; Score 24; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGW 11
: |||
Db 4 PGW 6

RESULT 12
COXO RAT
ID COXO RAT STANDARD; PRT; 10 AA.
AC P80432;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIC, mitochondrial (BC 1.9.3.1)
DE (VIIC) (Fragment).
GN COX7C OR COX7C1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart, and Liver;
RX MEDLINE=95324529; PubMed=7601105;
RX Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;
RT "Cytochrome c oxidase in developing rat heart. Enzymic properties and
RT amino-terminal sequences suggest identity of the fetal heart and the
RT adult liver isoform".
RL Eur. J. Biochem. 230:235-241(1995).
CC -1- FUNCTION: This protein is one of the nuclear-coded polypeptide
CC chains of cytochrome c oxidase, the terminal oxidase in
CC mitochondrial electron transport.
CC -1- CATALYTIC ACTIVITY: 4 ferri-cytochrome c + O(2) = 4 ferri-cytochrome
CC c + 2 H(2)O.
CC -1- SIMILARITY: Belongs to the cytochrome c oxidase VIIC family.
CC PIR; S65388; S65388.
KW Oxidoreductase; Mitochondrion.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1117 MW; 126DE767687B1B0B CRC64;

Query Match 32.4%; Score 23; DB 1; Length 10;
Best Local Similarity 71.4%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 6 HY--GPG 10
: |||
Db 2 HYERGPG 8

RESULT 13
COXO THUB
ID COXO THUB STANDARD; PRT; 10 AA.
AC P80982;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Cytochrome c oxidase polypeptide VIIC (BC 1.9.3.1) (Fragment).
OS Thunnus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart, and Liver;

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RX MEDLINE=97454291; PubMed=9310366;
 RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
 RA Kadabach B.;
 RT "The subunit structure of cytochrome-c oxidase from tuna heart and
 RT liver";
 RL Eur J Biochem. 248:99-103(1997).
 CC
 CC -1- FUNCTION: This protein is one of the nuclear-coded polypeptide
 CC chains of cytochrome c oxidase, the terminal oxidase in
 CC mitochondrial electron transport.
 CC -1- CATALYTIC ACTIVITY: 4 ferricytochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -1- SIMILARITY: Belongs to the cytochrome c oxidase VIIC family.
 DR PIR; S77990; S77990.
 KM Oxidoreductase; inner membrane; Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1059 MW; 126DE676787B1DCB CRC64;

 Query Match 32.4%; Score 23; DB 1; Length 10;
 Best Local Similarity 71.4%; Pred. No. 3.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 6 HY-GPG 10
 Db 2 HYAEGPG 8

RESULT 14
 HTF1_PERAM STANDARD; PRT; 8 AA.
 AC P04548;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypertrihaloemic factor I (Neuropeptide M-I) (Perrilametin CC-I)
 DE (Pea-CAH-I) (LED-CC-I) (Hypertrihaloemic neuropeptide I).
 OS Periplaneta americana (American cockroach).
 OS Lepidoptera: Decemlineata (Colorado potato beetle), and
 OS Blattella orientalis (Oriental cockroach).
 OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neuroptera; Neuroptera; Dictyoptera; Blattaria; Blattodea;
 OC Blattellidae; Periplaneta.
 OC NCBI_TaxID=6978, 7539, 6976;
 OK
 RN
 RN
 RP SEQUENCE.
 RC SPECIES=P. americana;
 RX MEDLINE=85046530; PubMed=6548628;
 RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
 RA Rinehart K.L. Jr.;
 RT "Structures of two cockroach neuropeptides assigned by fast atom
 RT bombardment mass spectrometry";
 RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
 RN
 RN
 RP SEQUENCE.
 RC SPECIES=P. americana;
 RX MEDLINE=84298179; PubMed=6591205;
 RA Scabroough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
 RA Miller C.A., Schooley D.A.;
 RT "Isolation and primary structure of two peptides with
 RT cardioacceleratory and hyperglycemic activity from the corpora
 RT cardiaca of Periplaneta americana";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
 RN
 RN
 RP SEQUENCE.
 RC SPECIES=L. decemlineata; TISSUE=Corpora cardiaca;
 RX MEDLINE=90160053; PubMed=2576128;
 RA Gaede G., Kallner R.;
 RT "The metabolic neuropeptides of the corpus cardiaca from the potato
 RT beetle and the American cockroach are identical";
 RL Peptides 10:1287-1289(1989).
 RN
 RN
 RP SEQUENCE.
 RC SPECIES=B. orientalis; TISSUE=Corpora cardiaca;

RX MEDLINE=90253659; PubMed=2340112;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary structures of hypertrihaloemic neuropeptides isolated from
 RT the corpora cardiaca of the cockroaches *Leucophaea maderae*,
 RT *Gromphadorhina portenosae*, *Blattella germanica* and *Blattella orientalis*
 RT and of the stick insect *Extatosoma tiaratum* assigned by tandem fast
 RT atom bombardment mass spectrometry";
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 CC
 CC -1- FUNCTION: Hypertrihaloemic factors are neuropeptides that
 CC elevate the level of trehalose in the hemolymph (trehalose is
 CC the major carbohydrate in the hemolymph of insects).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.
 DR PIR; A05169; A05169.
 DR PIR; A44960; A44960.
 DR PIR; A49823; A49823.
 DR PIR; S08995; S08995.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KM Neuropeptide; Amidation; Pyroglutamate carboxylic acid.
 FT MOD_RES 1 1
 FT MOD_RES 8 8
 FT MOD_RES 1 1
 SQ SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;

 Query Match 31.0%; Score 22; DB 1; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 HYGPW 11
 Db 3 NESPNW 8

RESULT 15
 HTF1_TENMO STANDARD; PRT; 8 AA.
 AC P25419;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypertrihaloemic factor (HOTH) (Hypertrihaloemic neuropeptide).
 OS Tenebrio molitor (Yellow mealworm), and
 OS Zophobas rugipes.
 OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neuroptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
 OC Tenebrionidae; Tenebrio.
 OC NCBI_TaxID=7067, 7075;
 OK
 RN
 RN
 RP SEQUENCE.
 RC SPECIES=T. molitor, and Z. rugipes;
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=90341081; PubMed=2381871;
 RA Gaede G., Rosinski G.;
 RT "The primary structure of the hypertrihaloemic neuropeptide from
 RT tenebrionid beetles: a novel member of the AKH/RPCH family";
 RL Peptides 11:455-459(1990).
 CC
 CC -1- FUNCTION: Hypertrihaloemic factors are neuropeptides that
 CC elevate the level of trehalose in the hemolymph (trehalose is the
 CC major carbohydrate in the hemolymph of insects).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.
 DR PIR; A43976; A43976.
 DR PIR; B43976; B43976.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KM Neuropeptide; Amidation; Pyroglutamate carboxylic acid.
 FT MOD_RES 1 1
 FT MOD_RES 8 8
 FT MOD_RES 1 1
 SQ SEQUENCE 8 AA; 1005 MW; 86745775B9C44736 CRC64;

 Query Match 31.0%; Score 22; DB 1; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 HYGPWM 11
 DB 3 NPSPMW 8

RESULT 16
 GONI_PETWA STANDARD; PRT; 10 AA.
 ID GONI_PETWA
 AC P04378;
 DT 20-MAR-1987 (Rel. 04, Last sequence update)
 DT 20-MAR-1987 (Rel. 04, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GNRH-I)
 DE (Lutiberin I).
 OS Petromyzon marinus (Sea lamprey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 OC Petromyzontiformes; Petromyzontidae; Petromyzon.
 OX NCBI_Taxid=7757;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=86168192; PubMed=3514603;
 RA Sherwood N.M., Sower S.A., Marshak D.R., Fraser B.A., Brownstein M.J.;
 RT "Primary structure of gonadotropin-releasing hormone from lamprey
 brain.";
 RT J. Biol. Chem. 261:4812-4819(1986).
 CC -1- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
 the secretion of both luteinizing and follicle-stimulating
 hormones.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the GNRH family.
 DR PIR; A01412; RHMWS.
 DR InterPro; IPR002012; GNRH.
 DR Pfam; PF00446; GNRH; 1.
 DR PROSITE; PS00473; GNRH; 1.
 KW Hormone; Amidation; Hypothalamus; Pyroglutamate carboxylic acid.
 FT MOD_RES 1 10
 FT AMIDATION.
 FT MOD_RES 10 10
 FT AMIDATION.
 SQ SEQUENCE 10 AA; 1244 MW; 1A4B36237B17355B CRC64;

Query Match 31.0%; Score 22; DB 1; Length 10;
 Best Local Similarity 42.9%; Pred. No. 5.2e+02;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 KHYGPWM 11
 DB 1 QHYSLEW 7

RESULT 17
 CORZ_PERAM STANDARD; PRT; 11 AA.
 ID CORZ_PERAM
 AC P1496;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Corazonin.
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
 OC Blattellidae; Periplaneta.
 OX NCBI_Taxid=6978;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=89325572; PubMed=2753132;
 RA Venetura J.A.;
 RT "Isolation and structure of corazonin, a cardioactive peptide from
 the American cockroach.";
 RT FEBS Lett. 250:231-234(1989).
 CC -1- FUNCTION: Cardioactive peptide. Corazonin is probably involved
 in the physiological regulation of the heart beat.

CC -1- SUBCELLULAR LOCATION: Secreted.
 DR PIR; S05002; S05002.
 KW Neuropeptide; Amidation; Pyroglutamate carboxylic acid.
 FT MOD_RES 1 1
 FT PYROGLUTAMATE CARBOXYLIC ACID.
 FT MOD_RES 11 11
 FT AMIDATION.
 SQ SEQUENCE 11 AA; 1387 MW; C7CF32D6415AB46 CRC64;

Query Match 31.0%; Score 22; DB 1; Length 11;
 Best Local Similarity 60.0%; Pred. No. 5.7e+02;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 YGPWM 11
 DB 5 YSRGW 9

RESULT 18
 BOWL_PSEGU STANDARD; PRT; 13 AA.
 ID BOWL_PSEGU
 AC P42951;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Bombesin-like peptide I (PG-I).
 OS Pseudophryne guentheri (Guenther's toadlet).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 CC Myobatrachinae; Pseudophryne.
 OX NCBI_Taxid=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erpagner V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 the Australian frog Pseudophryne guentheri.";
 RT Peptides 11:299-304(1990).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Skin.
 CC -1- SIMILARITY: Belongs to the bombesin/neuromedin B/ratanensin
 family.
 DR PIR; A60409; A60409.
 DR InterPro; IPR000874; Bombesin.
 DR Pfam; PF02044; Bombesin; 1.
 DR PROSITE; PS00257; BOMBESIN; 1.
 KW Amphibian defense peptide; Bombesin family; Amidation;
 KW Pyroglutamate carboxylic acid.
 FT MOD_RES 1 1
 FT AMIDATION.
 FT MOD_RES 13 13
 FT AMIDATION.
 SQ SEQUENCE 13 AA; 1372 MW; D6DE0D24BD98C366 CRC64;

Query Match 31.0%; Score 22; DB 1; Length 13;
 Best Local Similarity 75.0%; Pred. No. 6.8e+02;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 GPGWM 11
 DB 4 GPGW 7

RESULT 19
 AKHG_GRYBI STANDARD; PRT; 8 AA.
 ID AKHG_GRYBI
 AC P14086;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Adipokinetic hormone G (AKH-G) (RO II).
 OS Gryllus bimaculatus (Two-spotted cricket), and
 OS Romalea microptera (Lubber grasshopper).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Gryllota; Gryllidae; Gryllinae;
 OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;

OC Gryllus.
 OX NCBI_TaxID=6999, 7007;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=G. bimaculatus; TISSUE=Corpora cardiaca;
 RX MEDLINE=88106553; PubMed=3426616;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary sequence analysis by fast atom bombardment mass spectrometry
 of a peptide with adipokinetic activity from the corpora cardiaca of
 the cricket Gryllus bimaculatus.";
 RL Biochem. Biophys. Res. Commun. 149:908-914(1987).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=R. microptera; TISSUE=Corpora cardiaca;
 RX MEDLINE=89145002; PubMed=3226948;
 RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
 RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
 the lubber grasshopper, Romalea microptera.";
 RL Peptides 9:681-688(1988).
 CC -1- FUNCTION: This hormone, released from cells in the corpora
 cardiaca after the beginning of flight, causes release of
 diglycerides from the fat body and then stimulates the flight
 muscles to use these diglycerides as an energy source.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1
 FT MOD RES 8 8
 FT MOD RES 8 8
 SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;
 QY 6 HYGPGW 11
 DB 3 NRTSGW 8
 Query Match 28.2%; Score 20; DB 1; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 RESULT 20
 AKH LIBAU STANDARD; PRT; 8 AA.
 ID AKH LIBAU STANDARD; PRT; 8 AA.
 AC P25718;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Adipokinetic hormone (AKH).
 OS Libellula auripennis (Skimmer dragonfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
 OX NCBI_TaxID=6966;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=90359055; PubMed=2390213;
 RA Gaede G.;
 RT "The putative ancestral peptide of the adipokinetic/red-pigment-
 concentrating hormone family isolated and sequenced from a
 dragonfly.";
 RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).
 CC -1- FUNCTION: This hormone, released from cells in the corpora
 cardiaca after the beginning of flight, causes release of
 diglycerides from the fat body and then stimulates the flight
 muscles to use these diglycerides as an energy source.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1
 FT MOD RES 10 10
 FT MOD RES 10 10
 SQ SEQUENCE 10 AA; 1163 MW; 056236745771A9C4 CRC64;
 QY 6 HYGPGW 11
 DB 3 NRTSGW 8
 Query Match 28.2%; Score 20; DB 1; Length 10;
 Best Local Similarity 33.3%; Pred. No. 1.2e+03;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 RESULT 22
 NUDM CANFA STANDARD; PRT; 12 AA.
 ID NUDM CANFA STANDARD; PRT; 12 AA.
 AC P54713;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE NADH-ubiquinone oxidoreductase 42 kDa subunit (EC 1.6.5.3)
 DE (EC 1.6.99.3) (Complex I-42KD) (CI-42KD) (Fragment).
 OS NDUF410.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=98163340; PubMed=95504812;

FT MOD RES 1 1
 FT MOD RES 8 8
 SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;
 Query Match 28.2%; Score 20; DB 1; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 6 HYGPGW 11
 DB 3 NRTSGW 8
 Query Match 28.2%; Score 20; DB 1; Length 10;
 Best Local Similarity 33.3%; Pred. No. 1.2e+03;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 RESULT 21
 HTFL ROMMI STANDARD; PRT; 10 AA.
 ID HTFL ROMMI STANDARD; PRT; 10 AA.
 AC P18110;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE RO 1 (Hypertrehalosemic factor).
 OS Romalea microptera (lubber grasshopper).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
 OC Acridoidea; Romaleidae; Romalea.
 OX NCBI_TaxID=7007;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=89145002; PubMed=3226948;
 RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
 RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
 the lubber grasshopper, Romalea microptera.";
 RL Peptides 9:681-688(1988).
 CC -1- FUNCTION: Hypertrehalosemic factors are neuropeptides that
 elevate the level of trehalose in the hemolymph of insects.
 CC -1- major carbohydrate in the hemolymph of insects.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1
 FT MOD RES 10 10
 FT MOD RES 10 10
 SQ SEQUENCE 10 AA; 1163 MW; 056236745771A9C4 CRC64;
 QY 6 HYGPGW 11
 DB 3 NRTSGW 8
 Query Match 28.2%; Score 20; DB 1; Length 10;
 Best Local Similarity 33.3%; Pred. No. 1.2e+03;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 RESULT 22
 NUDM CANFA STANDARD; PRT; 12 AA.
 ID NUDM CANFA STANDARD; PRT; 12 AA.
 AC P54713;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE NADH-ubiquinone oxidoreductase 42 kDa subunit (EC 1.6.5.3)
 DE (EC 1.6.99.3) (Complex I-42KD) (CI-42KD) (Fragment).
 OS NDUF410.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=98163340; PubMed=95504812;

RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 RT dog heart proteins.";
 RL Electrophoresis 18:2795-2802(1997).
 CC -1- FUNCTION: Transfer of electrons from NADH to the respiratory
 chain. The immediate electron acceptor for the enzyme is believed
 to be ubiquinone.
 CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -1- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
 CC -1- COFACTOR: Binds 1 FAD per subunit.
 CC -1- SUBUNIT: Mammalian complex I is composed of 45 different subunits.
 CC This is a component of the hydrophobic protein fraction.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
 DR HSC-2DPAGE; P54713; DOG.
 KW Oxidoreductase; NAD; Ubiquinone; Flavoprotein; FAD; Mitochondrion.
 FT NON TER 12 12
 SQ SEQUENCE 12 AA; 1284 MW; 3CCDAE2B36EDD737 CRC64;

Query Match 28.2%; Score 20; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YGP 9
 DB 3 YGP 5

RESULT 23
 ID_RFI_CONSP STANDARD; PRT; 12 AA.
 AC P58805;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DB Conofamide-St.
 OS Conus spurius (Alphabet cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Scrobiconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=192919;

RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=21605839; PubMed=11738233;
 RA Malillo M., Aguilar M.B., Lopez-Yera E., Craig A.G., Bulaj G.,
 RA Olivera B.M., Helmer de la Coteria E.P.;
 RT "Conofamide, a Conus venom peptide belonging to the Rfamde family of
 RT neuropeptides.";
 RL Toxicon 40:401-407(2002).
 CC -1- FUNCTION: Causes hyperactivity in mice.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- MASS SPECTROMETRY: MW=1454.8; METHOD=Electrospray.
 CC -1- SIMILARITY: Belongs to the PARF (PMTamide related peptide)
 CC family.
 KW Neurotoxin; Toxin; Amidation.
 FT MOD RES 12 12
 SQ SEQUENCE 12 AA; 1456 MW; 2510671EA9D772D3 CRC64;

Query Match 27.5%; Score 19.5; DB 1; Length 12;
 Best Local Similarity 60.0%; Pred. No. 1.7e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 8 GP-GW 11
 DB 1 GP-GW 5
 RESULT 24
 HTF2_PERRAM STANDARD; PRT; 8 AA.
 ID HTF2_PERRAM
 AC P04549;
 DT 13-AUG-1987 (Rel. 05, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hyperetretaloasemic factor II (Neuropeptide M-II) (Periplaneta CC-2)
 DB (Pa-CH-II) (Ld-CC-II) (Hyperetretaloasemic neuropeptide II).
 OS Periplaneta americana (American cockroach).
 OS Lepidoptera decemlineata (Colorado potato beetle), and
 OS Blattella orientalis (Oriental cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
 CC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978; 7539; 6976;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE=85046530; PubMed=6548628;
 RA Witten J.V., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
 RA Rinehart K.L., Jr.;
 RT "Structures of two cockroach neuropeptides assigned by fast atom
 RT bombardment mass spectrometry.";
 RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE=84298179; PubMed=6591205;
 RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
 RA Miller C.A., Schooley D.A.;
 RT "Isolation and primary structure of two peptides with
 RT cardioacceleratory and hyperglycemic activity from the corpora
 RT cardiaca of Periplaneta americana.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
 RX MEDLINE=90160053; PubMed=2576128;
 RA Gaede G., Keilner R.;
 RT "The metabolic neuropeptides of the corpus cardiaca from the potato
 RT beetle and the American cockroach are identical.";
 RL Peptides 10:1287-1289(1989).
 RN [4]
 RP SEQUENCE.
 RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
 RX MEDLINE=90253659; PubMed=2340112;
 RA Gaede G., Rinehart K.L., Jr.;
 RT "Primary structures of hyperetretaloasemic neuropeptides isolated from
 RT the corpora cardiaca of the cockroaches Leucophaea maderae,
 RT Gryllodromia portensis, Blattella germanica and Blattella orientalis
 RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
 RT atom bombardment mass spectrometry.";
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 CC -1- FUNCTION: Hyperetretaloasemic factors are neuropeptides that
 CC elevate the level of trehalose in the hemolymph (trehalose is the
 CC major carbohydrate in the hemolymph of insects).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the AKH / HTH / RCH family.
 DR PIR; B44960; B44960.
 DR PIR; B49823; B49823.
 DR PIR; S08996; S08996.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1
 SQ SEQUENCE 8 AA; 1006 MW; 66745771A9D1A736 CRC64;

Query Match 26.8%; Score 19; DB 1; Length 8;
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 YGP 11
 DB 4 FT-PW 8

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RESULT 25
GN3 PETMA STANDARD; PRT; 10 AA.
ID GN3 PETMA STANDARD; PRT; 10 AA.
AC P30938;
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadolibetin III (Gonadotropin-releasing hormone III) (GnRH-III)
DE (Luliberin III).
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperartia;
OC Petromyzoniformes; Petromyzonidae; Petromyzon.
OX NCBI_TaxID=757;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RA MEDLINE=93178316; PubMed=8440174;
RA Sower S.A., Chiang Y.-C., Lovas S., Conlon J.M.;
RT "Primary structure and biological activity of a third gonadotropin-
RT releasing hormone from lamprey brain."
RL Endocrinology 132:1125-1131(1993).
CC -1- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
CC the secretion of both luteinizing and follicle-stimulating
CC hormones.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the GnRH family.
DR InterPro: IPR002012; GnRH.
DR Pfam: PF00446; GnRH; 1.
DR PROSITE: PS00473; GnRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyroglutamate carboxylic acid.
FT MOD RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.
FT MOD RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1277 MW; 284B36237A1F5A3 CRC64;

Query Match 26.8%; Score 19; DB 1; Length 10;
Best Local Similarity 28.6%; Pred. No. 1.7e+03;
Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 KHYGPGM 11
DB 1 QHMSHW 7

RESULT 26
HTF2 CARMO STANDARD; PRT; 10 AA.
ID HTF2 CARMO STANDARD; PRT; 10 AA.
AC P11385;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrehalosaemic factor II (HTF-II) (HRTII-II) (Hypertrehalosaemic
DE neuropeptide II).
OS Carausius morosus (Indian stick insect), and
OS Extatosoma tiaratum (Stick insect).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Phasmatodea; Euphasmatodea;
OC Heteromulidae; Carausius.
OX NCBI_TaxID=7022, 7024;
RN [1]
RP SEQUENCE.
RC SPECIES=C. morosus; TISSUE=Corpora cardiaca;
RA MEDLINE=87157103; PubMed=388078;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structure of the hypertrehalosaemic factor II from the
RT corpus cardiaca of the Indian stick insect, Carausius morosus,
RT determined by fast atom bombardment mass spectrometry."
RL Biol. Chem. Hoppe-Seyler 368:67-75(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=E. tiaratum; TISSUE=Corpora cardiaca;
RA MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehalosaemic neuropeptides isolated from

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RT the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Gryllotalpa orientalis, Blatella germanica and Blatella orientalis
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT atom bombardment mass spectrometry."
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
RN [3]
RP CARBOHYDRATE-LINKAGE SITE.
RC SPECIES=C. morosus; TISSUE=Corpora cardiaca;
RA MEDLINE=93129188; PubMed=1482345;
RA Gaede G., Kellner R., Rinehart K.L. Jr., Proefke M.L.;
RT "A tryptophan-substituted member of the AKH/RPCH family isolated from
RT a stick insect corpus cardiaca."
RL Biochem. Biophys. Res. Commun. 189:1303-1309(1992).
CC -1- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph (trehalose is the
CC major carbohydrate in the hemolymph of insects).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTII / RPCH family.
DR PIR: A31571, A31571.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Glycoprotein; Pyroglutamate carboxylic acid.
FT MOD RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.
FT MOD RES 8 8 C-LINKED (MAN) (PROBABLE).
FT MOD RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1164 MW; 98903674577A9D1 CRC64;

Query Match 26.8%; Score 19; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.7e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 YGPGM 11
DB 4 FTFPM 8

RESULT 27
HTF HELZE STANDARD; PRT; 10 AA.
ID HTF HELZE STANDARD; PRT; 10 AA.
AC P16353;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrehalosaemic hormone (Hez-HRTII).
OS Heliothis zea (Corn earworm) (Bollworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Heliothinae; Helioverpa.
OX NCBI_TaxID=7113;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RA MEDLINE=88326324; PubMed=3415690;
RA Uffe H., Kaina A.K., Riley C.T., Frazer B.A., Bird T.G.,
RA Tseng C.M., Zhang Y.S., Hayes D.K.;
RT "Isolation and primary structure of a neuropeptide hormone from
RT Heliothis zea with hypertrehalosaemic and adipo-kinetic activities."
RL Biochem. Biophys. Res. Commun. 155:344-350(1988).
CC -1- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph (trehalose is the
CC major carbohydrate in the hemolymph of insects).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTII / RPCH family.
DR PIR: A31571, A31571.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyroglutamate carboxylic acid.
FT MOD RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.
FT MOD RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1096 MW; 8E70367865A5B9D1 CRC64;

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Query Match      26.8%; Score 19; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.7e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 YGPGW 11
   : ||
   : ||
Db 4 FSSGW 8

RESULT 28
CS15_BACSU STANDARD; PRT; 11 AA.
ID CS15_BACSU
AC P81095;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cold shock protein CS15 (11 kDa cold shock protein) (Fragment).
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE.
RC STRAIN=168 / JH642;
RA Graumann P.L., Schmid R., Marahiel M.A.;
RL Submitted (OCT-1997) to Swiss-Prot.
RN [2]
RP CHARACTERIZATION.
RC STRAIN=168 / JH642;
RX MEDLINE=96345629; PubMed=8755892;
RT "Cold shock stress-induced proteins in Bacillus subtilis.";
RL J. Bacteriol. 178:4611-4619(1996).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- INDUCTION: In response to low temperature.
CC -1- CAUTION: Could not be found in the genome of B. subtilis 168.
FT NON TER 11
SQ SEQUENCE 11 AA; 1360 MW; 15F6ECE6322C330 CRC64;

Query Match      25.4%; Score 18; DB 1; Length 11;
Best Local Similarity 42.9%; Pred. No. 2.8e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NFKLKHV 7
   : |||
   : |||
Db 3 NIKVKEP 9

RESULT 29
MTA_CAMDR STANDARD; PRT; 13 AA.
ID MTA_CAMDR
AC P01198;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Melanotropin alpha (Alpha-MSH).
OS Camelus dromedarius (Dromedary) (Arabic camel), and
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838, 9796;
RN [1]
RP SEQUENCE.
RC SPECIES=C.dromedarius;
RX MEDLINE=75146434; PubMed=1125179;
RA Li C.H., Danho M.O., Chung D., Rao A.J.;
RT "Isolation, characterization, and amino acid sequence of
RT melanotropins from camel pituitary glands.";
RL Biochemistry 14:947-952(1975).
RN [2]
RP SEQUENCE.
RC SPECIES=Horse; TISSUE=Plutitary;
RA Dixon J.S., Li C.H.;
RT "The isolation and structure of alpha-melanocyte-stimulating hormone

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RT from horse pituitaries.";
RL J. Am. Chem. Soc. 82:4568-4572(1960).
CC -1- SIMILARITY: Belongs to the POMC family.
DR PIR; A01464; MTCMAD.
DR PIR; A91785; MTHOAD.
DR InterPro; IPR001941; Mcoitin_ACTH.
DR Pfam; PF00976; ACTH_domain; 1.
KW Hormone; Acetylation; Amidation.
FT MOD_RES 1
FT MOD_RES 1 ACETYLATION (IN ABOUT 50% OF CAMEL
FT MOD_RES 1 MOLECULES).
FT MOD_RES 13
FT MOD_RES 13 AMIDATION.
SQ SEQUENCE 13 AA; 1624 MW; FF991CA958B09C1 CRC64;

Query Match      25.4%; Score 18; DB 1; Length 13;
Best Local Similarity 14.3%; Pred. No. 3.3e+03;
Matches 1; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 NFKLKHV 7
   : |||
   : |||
Db 1 SYSMEHF 7

RESULT 30
SA2A_ONCMY STANDARD; PRT; 13 AA.
ID SA2A_ONCMY
AC P82238;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Salmocidin 2A (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Proactanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Serum.
RA Henry M.A., Secombes C.J.;
RT "Purification and partial characterization of antibacterial peptides
RT from rainbow trout, Oncorhynchus mykiss.";
RL Submitted (DEC-1999) to Swiss-Prot.
CC -1- FUNCTION: Antibacterial activity against Gram-negative bacteria.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Plasma serum.
KW Antibiotic.
FT NON TER 13
SQ SEQUENCE 13 AA; 1416 MW; 5FFB792AFC645873 CRC64;

Query Match      25.4%; Score 18; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FKLKHV 7
   : |||
   : |||
Db 3 FVLKGY 8

RESULT 31
SA2B_ONCMY STANDARD; PRT; 13 AA.
ID SA2B_ONCMY
AC P82239;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Salmocidin 2B (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Proactanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE, AND FUNCTION.

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RC TISSUE=Serum;
RA Henry M.A., Secombes C.J.,
RT "Purification and partial characterization of antibacterial peptides
from rainbow trout, *Oncorhynchus mykiss*,"
RL Submitted (DEC-1999) to Swiss-Pat.
CC -1- FUNCTION: Antibacterial activity against Gram-negative bacteria.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Plasma serum.
KM Antibiotic.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1400 MW; 5FFB792AEABE5873 CRC64;

Query Match 25.4%; Score 18; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 3.3e-03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FVLKGY 7
DB 3 FVLKGY 8

RESULT 32
UN12_CLOPA STANDARD; PRT; 13 AA.
AC P81353;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Unknown protein CP 12 from 2D-page (Fragment).
OC Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxId=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=MS;
RX MEDLINE=98291870; PubMed=962918;
RA Flensburg R., Skjeldal L.,
RT "Two-dimensional gel electrophoresis separation and N-terminal
sequence analysis of proteins from *Clostridium pasteurianum* WS,"
RL Electrophoresis 19:802-806(1998).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 5.8, ITS MW IS: 42.7 kDa.
FT VARIANT 4 4 L -> V.
FT NON_TER 5 5 Q -> I.
SQ SEQUENCE 13 AA; 1465 MW; 70A9B9845SD405B CRC64;

Query Match 25.4%; Score 18; DB 1; Length 13;
Best Local Similarity 33.3%; Pred. No. 3.3e-03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 FVLKGYPG 10
DB 2 VYLGEINPG 10

RESULT 33
LPM_ECOLI STANDARD; PRT; 14 AA.
AC P03053;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE TYP operon leader peptide.
GN TRPL OR TRPE OR B1265 OR C5494 OR Z2545 OR ECS1837 OR SFL1268 OR
S4805.
OS *Escherichia coli*,
OS *Escherichia coli* O6,
OS *Escherichia coli* O157:H7, and
OS *Shigella flexneri*.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; *Escherichia*.

OX NCBI_TaxId=562, 217992, 83334, 623;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=2210258; PubMed=7036627;
RA Yanofsky C., Platt T., Crawford I.P., Nichols B.P., Christie G.E.,
RA Horowitz H., van Gieumpt M., Wu A.M.,
RT "The complete nucleotide sequence of the tryptophan operon of
RT *Escherichia coli*,"
RL Nucleic Acids Res. 9:6647-6668(1981).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=76240562; PubMed=781271;
RA Squires C., Lee F., Bertrand K., Squires C.L., Bronson M.J.,
RA Yanofsky C.,
RT "Nucleotide sequence of the 5' end of tryptophan messenger RNA of
RT *Escherichia coli*,"
RL J. Mol. Biol. 103:351-381(1976).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=80101455; PubMed=118451;
RA Oxender D.L., Zurawski G., Yanofsky C.,
RT "Attenuation in the *Escherichia coli* tryptophan operon: role of RNA
RT secondary structure involving the tryptophan codon region,"
RL Proc. Natl. Acad. Sci. U.S.A. 76:5524-5528(1979).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12 / MG1655;
RX MEDLINE=97426817; PubMed=9278503;
RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.,
RT "The complete genome sequence of *Escherichia coli* K-12,"
RL Science 277:1453-1474(1997).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=OG:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett H.A.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley R.L.T., Domeneberg M.S., Blatner F.R.,
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic *Escherichia coli*,"
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
RN [6]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=1206511;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Poramouzis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blatner F.R.,
RT "Genome sequence of enterohaemorrhagic *Escherichia coli* O157:H7,"
RL Nature 409:529-533(2001).
RN [7]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Onishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Itoe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shida T., Hattori M., Shingawa H.,
RT "Complete genome sequence of enterohaemorrhagic *Escherichia coli*
RT O157:H7 and genomic comparison with a laboratory strain K-12,"
RL DNA Res. 8:11-22(2001).
RN [8]
RP SEQUENCE FROM N.A.

CC SPECIES-S.flexneri; STRAIN=301 / Serotype 2a;
 RX MEDLINE=2272406; PubMed=12384590;
 RA Jin O., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
 RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
 RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
 RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
 RA Yu J.;
 RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
 RT through comparison with genomes of Escherichia coli K12 and O157.";
 RL Nucleic Acids Res. 30:4432-4441(2002).
 RN [9]
 RP SEQUENCE FROM N.A.
 RC SPECIES-S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;
 RX MEDLINE=22590274; PubMed=12704152; Venkatesan M.M., Deng W.,
 RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
 RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
 RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
 RA Schwartz D.C., Blattner F.R.;
 RT "Complete genome sequence and comparative genomics of Shigella
 RT flexneri serotype 2a strain 2457T.";
 RL Infect. Immun. 71:2775-2786(2003).
 CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
 CC OF TRYPTOPHAN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR EMBL; J01714; AAA57296.1; -;
 DR EMBL; A04494; CAA00361.1; -;
 DR EMBL; AE000224; AAC74347.1; -;
 DR EMBL; AE016760; AAN80196.1; -;
 DR EMBL; AE005380; AAG56550.1; -;
 DR EMBL; AP002556; BAB35260.1; -;
 DR EMBL; AE015153; AAN42881.1; -;
 DR EMBL; AE016982; AAP16766.1; -;
 DR PIR; A03589; LFEWC.
 DR PIR; B85761; B85761.
 DR PIR; B90858; E90858.
 DR Ecogene; EG11274; trpL.
 KW Tryptophan biosynthesis; Leader peptide; Complete proteome.
 SQ SEQUENCE 14 AA; 1723 MW; 5B793063E804A37 CRC64;
 QY Query Match 25.4%; Score 18; DB 1; Length 14;
 Best Local Similarity 50.0%; Pred. No. 3.6e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 4; Gaps 1;
 DB 2 FKLXHGPGM 11
 5 FVLK---GM 10
 RESULT 34
 MCR2 METTM STANDARD; PRT; 14 AA.
 ID MCR2 METTM STANDARD; PRT; 14 AA.
 AC P58816;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Methyl-coenzyme M reductase II gamma subunit (EC 1.8.-.-) (MCR II
 DE gamma) (Fragment).
 GN MRCG
 OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanobacter.
 OX NCBI_TaxID=79929;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91099370; PubMed=2269306;

RA Rospert S., Linder D., Ellermann J., Thauer R.K.;
 RT "Two genetically distinct methyl-coenzyme M reductases in
 RT Methanobacterium thermoautotrophicum strain Marburg and delta H.";
 RL Eur. J. Biochem. 194:871-877(1990).
 CC -!- FUNCTION: Reduction of methyl-coenzyme M (2-(methylthio)
 CC ethanesulfonic acid) with 7-mercaptopyruvylthioneine phosphate
 CC to methane and an heterodisulfide.
 CC -!- CATALYTIC ACTIVITY: CH(3)-S-CoM + H-S-HTP = CH(4) + CoM-S-S-HTP.
 CC -!- COFACTOR: Binds 2 coenzyme F430 noncovalently per hexamer.
 CC Coenzyme F430 is a yellow nickel porphyrinoid.
 CC -!- PATHWAY: Methanogenesis; last step.
 CC -!- SUBUNIT: Hexamer of two alpha, two beta, and two gamma chains.
 CC -!- DEVELOPMENTAL STAGE: THERE ARE TWO MCR COMPLEXES IN THIS BACTERIA.
 CC MCR II IS EXPRESSED IN THE EARLY GROWTH PHASE. LATE GROWTH CELLS
 CC CONTAINS MOSTLY MCR I.
 DR PIR; B69017; E69017.
 KW Methanogenesis; Oxidoreductase; Multigene family.
 FT INIT MET 0
 FT NON TER 0
 SQ SEQUENCE 14 AA; 1557 MW; 97B9439C4223B871 CRC64;
 QY Query Match 25.4%; Score 18; DB 1; Length 14;
 Best Local Similarity 75.0%; Pred. No. 3.6e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DB 7 YGPG 10
 6 YTPG 9
 RESULT 35
 ALL1 CYDPO STANDARD; PRT; 8 AA.
 ID ALL1 CYDPO STANDARD; PRT; 8 AA.
 AC P82152;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cydiastratin 1.
 OS Cydia pomonella (Coddling moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preyrygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Tortricoidae; Tortricidae; Olethreutinae; Cydia.
 OX NCBI_TaxID=82600;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Larva;
 RX MEDLINE=96054539; PubMed=9392829;
 RA Davey H., Johnsen A.H., Maestri U.-L., Scott A.G., Winstanley D.,
 RA Davey M., East P.D., Thorpe A.;
 RT "Lepidopteran peptides of the allatostatin superfamily.";
 RT Peptides 18:1301-1309(1997).
 CC -!- SIMILARITY: Belongs to the allatostatin family.
 CC Neuropeptide; Amidation.
 KW MOD RES 8
 FT MOD RES 8
 SQ SEQUENCE 8 AA; 934 MW; C82879C45B51F775 CRC64;
 QY Query Match 23.9%; Score 17; DB 1; Length 8;
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 DB 6 HYPG 10
 3 HYPG 7
 RESULT 36
 CCKN MACEU STANDARD; PRT; 8 AA.
 ID CCKN MACEU STANDARD; PRT; 8 AA.
 AC P30369;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cholecystokinin (CCK).

GN CCK.
 OS Mactopus eugeni (Tammam wallaby), and
 OS Dasyurus viverrinus (Southeastern quoll).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
 RX NCBI_TaxID=9315, 9279;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=M. eugeni, and D. viverrinus;
 RC TISSUE=Brain;
 RX MEDLINE=8834141; PubMed=3375140;
 RA Fan Z.W., Eng J., Shaw G., Yalow R.S.;
 RT "Cholecystokinin octapeptide purified from brains of Australian
 RT marsupials";
 RL Peptides 9:429-431(1988).
 CC -1- FUNCTION: This peptide hormone induces gall bladder contraction
 CC and the release of pancreatic enzymes in the gut. Its function in
 CC the brain is not clear.
 CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR PIR; A43001; A43001.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; 1.
 KW Amidation; Sulfation; Hormone.
 FT MOD RES 2
 FT MOD RES 2
 FT MOD RES 2
 SQ SEQUENCE 8 AA; 1064 MW; DDCAA68378768B5A CRC64;

Query Match 23.9%; Score 17; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GW 11
 DB 4 GW 5

RESULT 37
 ID UP06 MOUSE STANDARD; PRT; 8 AA.
 AC P38644;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of fibroblasts (P50) (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Fibroblast;
 RC MEDLINE=9500907; PubMed=7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins
 RT using preparative two-dimensional gel electrophoresis";
 RL Electrophoresis 15:735-745(1994).
 DE -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 DE protein is: 5.2, its MW is: 50 kDa.
 CC NON TER 8
 CC SEQUENCE 8 AA; 817 MW; A35DD878676B05B1 CRC64;

Query Match 23.9%; Score 17; DB 1; Length 8;
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 HYPG 10
 DB 1 HSEPG 5

RESULT 38
 LIMP_LOCMI

ID LIMP_LOCMI STANDARD; PRT; 9 AA.
 AC P31799;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-OCT-1993 (Rel. 27, Last annotation update)
 DE Locustamycin inhibiting peptide (LOM-MIP).
 OS Locusta migratoria (migratory locust).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
 CC Acridoidea; Acrididae; Oedipodinae; Locusta.
 RX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92179466; PubMed=1796179;
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
 RT "Isolation, identification and synthesis of locustamycininhibiting
 RT peptide (LOM-MIP), a novel biologically active neuropeptide from
 RT Locusta migratoria";
 RL Regul. Pept. 36:111-119(1991).
 CC -1- FUNCTION: Suppresses spontaneous contractions of the hindgut and
 CC oxidant.
 CC -1- TISSUE SPECIFICITY: Neurons located in two ventral cell clusters
 CC in the suboesophageal ganglion.
 DR PIR; A60065; AKLQIM.
 KW Amidation; Neuropeptide.
 FT MOD RES 9
 FT MOD RES 9
 FT MOD RES 9
 SQ SEQUENCE 9 AA; 1060 MW; 387D7DD4472AB6C3 CRC64;

Query Match 23.9%; Score 17; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GW 11
 DB 8 GW 9

RESULT 39
 ID BPP VIPAS STANDARD; PRT; 10 AA.
 AC P31351;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide (Angiotensin-converting
 DE enzyme inhibitor).
 OS Vipera aspis (aspis viper).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
 CC Viperidae; Viperinae; Vipera.
 RX NCBI_TaxID=8706;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RC MEDLINE=90382616; PubMed=2169439;
 RA Komori Y., Sugihara H.;
 RT "Characterization of a new inhibitor for angiotensin converting
 RT enzyme from the venom of Vipera aspis aspis";
 RL Int. J. Biochem. 22:767-771(1990).
 DE -1- FUNCTION: This peptide both inhibits the activity of the
 DE angiotensin-converting enzyme and enhances the action of
 DE bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 CC PIR; A60377; XASNPc.
 DR Hypotensive agent; Pyrrolidone carboxylic acid.
 KW MOD RES 1
 KW MOD RES 1
 KW MOD RES 1
 SQ SEQUENCE 10 AA; 1062 MW; 3B827C3237686773 CRC64;

Query Match 23.9%; Score 17; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.8e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GW 11

Db 2 GW 3

RESULT 40
CA12_LITCI STANDARD; PRT; 10 AA.
ID CA12_LITCI
AC P82086;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein 1.2/1.2Y4.
OS Litoria citropa (Australian blue mountains tree frog), and
OS Litoria splendida (Magnificent tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
NCBI_TaxID=94770, 30345;
[1]
RN NCB
RP SEQUENCE, AND MASS SPECTROMETRY (CAERULEIN 1.2 AND 1.2Y4).
RC SPECIES=L. citropa; TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A.; Bowie J.H.; Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue mountains tree frog Litoria citropa. Part 1. Sequence determination using electrospray mass spectrometry.";
RT Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
[2]
RN NCB
RP SEQUENCE, AND MASS SPECTROMETRY (CAERULEIN 1.2).
RC SPECIES=L. splendida; TISSUE=Skin secretion;
RX MEDLINE=20069371; PubMed=10601876;
RA Wabnitz P.A.; Bowie J.H.; Tyler M.J.; Wallace J.C.; Smith B.P.;
RT "Differences in the skin peptides of the male and female Australian tree frog Litoria splendida. The discovery of the aquatic male sex pheromone splendipherin, together with pheb caerulein and the antibiotic peptide caerin 1.10.";
RT Eur. J. Biochem. 267:269-275(2000).
RN NCB
RP FUNCTION: Hypotensive neuropeptide (probable).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin dorsal glands.
CC -1- PTM: Isoform 1.2Y4 differs from isoform 1.2 in not being sulfated.
CC -1- MASS SPECTROMETRY: MW=1366; METHOD=Electrospray.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro: IPR001651; Gastrin.
DR PROSITE: PS00259; GASTRIN; FALSE_NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyroglutamate carboxylic acid.
FT MOD_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1306 MW; 99DBFCD37861B5A CRC64;
Query Match 23.9%; Score 17; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 10 GW 11
6 GW 7

RESULT 41
CAER_LITXA STANDARD; PRT; 10 AA.
ID CAER_LITXA
AC P56264;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein.
OS Litoria xanthurus (Orange-thighed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
NCBI_TaxID=79697;
[1]
RN NCB
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=97374000; PubMed=9230483;
RA Steindorner S.T.; Waugh R.J.; Bowie J.H.; Wallace J.C.; Tyler M.J.;
RT "New caerin antibacterial peptides from the skin glands of the Australian tree frog Litoria xanthurus.";
RT J. Pept. Sci. 3:181-185(1997).
RN NCB
RP FUNCTION: Hypotensive neuropeptide.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin dorsal glands.
CC -1- MASS SPECTROMETRY: MW=1354; METHOD=FAB.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro: IPR001651; Gastrin.
DR PROSITE: PS00259; GASTRIN; 1.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyroglutamate carboxylic acid.
FT MOD_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1290 MW; 99DBF3837861B5A CRC64;
Query Match 23.9%; Score 17; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 10 GW 11
6 GW 7

RESULT 42
TNN1_SCYCA STANDARD; PRT; 10 AA.
ID TNN1_SCYCA
AC P08608;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Scyliorhinin I.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphi; Galeoidei; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
NCBI_TaxID=7830;
[1]
RN NCB
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=86192829; PubMed=2422058;
RA Conlon J.M.; Deacon C.F.; O'Toole L.; Thim L.;
RT "Scyliorhinin I and II: two novel tachykinins from dogfish gut.";
RT FEBS Lett. 200:111-116(1986).
[2]
RN NCB
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=93292508; PubMed=7685693;
RA Waugh D.; Wang Y.; Hazen N.; Balmert R.J.; Conlon J.M.;
RT "Primary structures and biological activities of substance-P-related peptides from the brain of the dogfish, Scyliorhinus canicula.";
RT Eur. J. Biochem. 214:469-474(1993).
RN NCB
RP FUNCTION: Tachykinins are active peptides which excite neurons, evoke behavioral responses, are potent vasodilators and secreteagogues, and contract (directly or indirectly) many smooth muscles.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the tachykinin family.
CC PIR: A24867; A24867.
DR InterPro: IPR002040; Tachy Neurokinin.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.

SQ SEQUENCE 10 AA; 1219 MW; D0602D6B59C33AA9 CRC64;
 Query Match 23.9%; Score 17; DB 1; Length 10;
 Best Local Similarity 75.0%; Pred. No. 3.8e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHVG 8
 DB 5 KFYG 8

RESULT 43

TXS1_AEDAE STANDARD; PRT; 10 AA.
 AC P42634;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Stalokinin I.
 OS Aedes aegypti (Yellowfever mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes.
 OC NCBI_TaxID=7159;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=Rockefeller; TISSUE=salivary gland;
 RX MEDLINE=94105119; PubMed=8278354;
 RA Champagne D.E., Ribeiro J.M.C.;
 RT "Stalokinin I and II: Vasodilatory tachykinins from the yellow fever
 mosquito Aedes aegypti."
 RL Proc. Natl. Acad. Sci. U.S.A. 91:138-142(1994).
 CC -1- FUNCTION: Vasodilatory peptide. May activate macrophages at the
 site of feeding.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the tachykinin family.
 DR InterPro: IPR002040; Tachy. Neurokinin.
 DR PROSITE: PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1145 MW; 3DCFDEB59C33AA8 CRC64;

Query Match 23.9%; Score 17; DB 1; Length 10;
 Best Local Similarity 75.0%; Pred. No. 3.8e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHVG 8
 DB 5 KFYG 8

RESULT 44

TXS2_AEDAE STANDARD; PRT; 10 AA.
 AC P42635;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Stalokinin II.
 OS Aedes aegypti (Yellowfever mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes.
 OC NCBI_TaxID=7159;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=Rockefeller; TISSUE=salivary gland;
 RX MEDLINE=94105119; PubMed=8278354;
 RA Champagne D.E., Ribeiro J.M.C.;
 RT "Stalokinin I and II: Vasodilatory tachykinins from the yellow fever
 mosquito Aedes aegypti."
 RL Proc. Natl. Acad. Sci. U.S.A. 91:138-142(1994).
 CC -1- FUNCTION: Vasodilatory peptide. May activate macrophages at the
 site of feeding.

Query Match 23.9%; Score 17; DB 1; Length 10;
 Best Local Similarity 75.0%; Pred. No. 3.8e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the tachykinin family.
 DR InterPro: IPR002040; Tachy. Neurokinin.
 DR PROSITE: PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1146 MW; 3DC77C6B59C33AA8 CRC64;

Query Match 23.9%; Score 17; DB 1; Length 10;
 Best Local Similarity 75.0%; Pred. No. 3.8e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHVG 8
 DB 5 KFYG 8

RESULT 45

UXA6_CHLTR STANDARD; PRT; 10 AA.
 AC P38007;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Unknown protein from 2D-page from elementary body (Fragment).
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OC NCBI_TaxID=613;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=L2/434/Bu;
 RA Bini L., Santucci A., Maggi B., Marzocchi B., Sanchez-Campillo M.,
 RA Comanducci M., Christensen G., Birkelund S., Vetreu E., Ratti G.,
 RA Pallini V.;
 RL Submitted (SEP-1994) to Swiss-Prot.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.44, ITS MW IS: 38.6 kDa.
 DR Sienna-2DPAGE; P38007; -.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1243 MW; DAD39A33304B5339 CRC64;

Query Match 23.9%; Score 17; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NFX 3
 DB 2 NFX 4

Search completed: August 30, 2004, 10:50:21
 Job time : 2.89527 secs

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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:41:54 ; Search time 3.30743 Seconds
(without alignments)
319.918 Million cell updates/sec

Title: US-09-720-469A-5

Perfect score: 71

Sequence: 1 NFKLKHVGPWM 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1638

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	39.4	8	2 A61348	red pigment-concen
2	28	39.4	10	2 A60421	hypertrehalosemic
3	28	39.4	10	2 S08997	hypertrehalosemic
4	28	39.4	10	2 S08998	hypertrehalosemic
5	28	39.4	10	2 A26381	hypertrehalosemic
6	26	36.6	8	2 S55310	adipokineic hormo
7	26	36.6	8	2 A58620	adipokineic hormo
8	26	36.6	10	1 RHAQ2	gonadoliberin II -
9	26	36.6	10	1 A61126	gonadoliberin II -
10	26	36.6	10	2 B46030	gonadoliberin II -
11	26	36.6	10	2 A46030	gonadoliberin II -
12	25	35.2	8	2 S15622	adipokineic hormo
13	25	35.2	8	2 A33955	adipokineic hormo
14	25	35.2	8	2 A58641	adipokineic hormo
15	25	35.2	8	2 S21663	neuropeptide - flo
16	25	35.2	10	2 B33995	hypertrehalosemic h
17	25	35.2	10	2 A21114	hypertrehalosemic h
18	25	35.2	10	2 S39030	gonadoliberin - ch
19	24	33.8	11	2 S70338	lysoyl-bradykinin -
20	24	33.8	14	2 PH1322	napin small chain
21	24	33.8	9	2 PT0288	Ig heavy chain DJ
22	23	32.4	10	2 S65388	cytochrome-c oxida
23	23	32.4	10	2 S77990	cytochrome-c oxida
24	23	32.4	11	2 PT0302	Ig heavy chain CRD
25	23	31.0	8	2 S08995	hypertrehalosemic
26	22	31.0	8	2 A49823	adipokineic hormo
27	22	31.0	8	2 A44860	neuropeptide led-C
28	22	31.0	8	2 A43976	hypertrehalosemic
29	22	31.0	8	2 B43976	hypertrehalosemic

30	22	31.0	8	2 A05169	neuropeptide M-I -
31	22	31.0	10	1 RHLMS	gonadoliberin - se
32	22	31.0	10	2 S53789	neuropeptide Pec-H
33	22	31.0	11	2 S05002	corazonin - Americ
34	22	31.0	13	2 A60409	bombesin-like pep
35	22	31.0	13	2 S23640	Ig kappa chain J s
36	22	31.0	14	2 S33802	chaperone, TCPI-re
37	22	29.6	11	2 PT0209	T-cell receptor al
38	21	29.6	13	2 PH1593	Ig H chain V-D-J r
39	21	29.6	14	2 S03530	Ig heavy chain J r
40	20	28.2	8	2 A28004	adipokineic hormo
41	20	28.2	8	2 S10596	adipokineic hormo
42	20	28.2	8	2 S11545	adipokineic hormo
43	20	28.2	8	2 PT0368	Ig gamma chain C r
44	20	28.2	12	2 PQ0786	NADH2 dehydrogenas
45	20	28.2	14	2 PQ0152	18K iron-sulfur pr

ALIGNMENTS

RESULT 1
A61348
red pigment-concentrating hormone - northern shrimp
N/Alternate names: blanching hormone
C/Species: Pandalus borealis (northern shrimp)
C/Date: 02-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
C/Accession: A61348; S07139
R/Fernlund, P.; Josefsson, L.
Science 177, 173-175, 1972
A/Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.
A/Reference number: A61348; PMID:7228738; PMID:5041363
A/Accession: A61348
A/Molecule type: protein
A/Residues: 1-8 <PERL>
R/Fernlund, P.
Biochim. Biophys. Acta 371, 304-311, 1974
A/Title: Structure of the red-pigment-concentrating hormone of the shrimp, Pandalus borealis
A/Reference number: S07139; PMID:75054965; PMID:4433569
A/Accession: S07139
A/Molecule type: protein
A/Residues: 15, 2-8 <PERL>
A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C/Comment: This neuropeptide, isolated from the eyestalks of the shrimp and active in pi
zed pigment-containing cells.
C/Superfamily: adipokineic hormone
C/Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyroglutami
F.1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F.8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 39.4%; Score 28; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 6 HYGPWM 11
DB 3 NFKLKHVGPWM 11

RESULT 2
A60421
hypertrehalosemic hormone - German cockroach
N/Alternate names: Bld-HrTH
C/Species: Blatella germanica (German cockroach)
C/Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 31-Oct-1997
C/Accession: A60421; S09137
R/Veenstra, J.A.; Camps, F.
Neuropeptides 15, 107-109, 1990
A/Title: Structure of the hypertrehalosemic neuropeptide of the German cockroach, Blatte
A/Reference number: A60421; PMID:91179584; PMID:2080017
A/Accession: A60421
A/Molecule type: protein
A/Residues: 1-10 <VEB>

R:Gaede, G.; Rinehart, K.L.
Biol.Chem. Hoppe-Seyler 371, 345-354, 1990
A:Title: Primary structures of hypertrichalosemic neuropeptides isolated from the corpora enthalis and of the stick insect *Extatosoma tiaratum* assigned by tandem fast atom bombardment
A:Reference number: S08995; MUID:90253659; PMID:2340112
A:Accession: S09137
A:Molecule type: protein
A:Residues: 1-10 <GAB>
C:Superfamily: adipoikinetin hormone
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F:10/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 39.4%; Score 28; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 HYGPWM 11
::|||

DB 3 NFSPGM 8

RESULT 3
S08997
Hypertrichalosemic neuropeptide Bld-HrTH - cockroach (*Gromphadorina portentosa*)
C:Species: *Gromphadorina portentosa*
C:Date: 30-Jun-1992 #sequence_revision 14-Sep-1994 #text_change 24-Oct-1997
C:Accession: S08997
R:Gaede, G.; Rinehart, K.L.
Biol.Chem. Hoppe-Seyler 371, 345-354, 1990
A:Title: Primary structures of hypertrichalosemic neuropeptides isolated from the corpora enthalis and of the stick insect *Extatosoma tiaratum* assigned by tandem fast atom bombardment
A:Reference number: S08995; MUID:90253659; PMID:2340112
A:Accession: S08997
A:Molecule type: protein
A:Residues: 1-10 <GAB>
C:Superfamily: adipoikinetin hormone
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F:10/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 39.4%; Score 28; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 HYGPWM 11
::|||

DB 3 NFSPGM 8

RESULT 4
S08998
Hypertrichalosemic neuropeptide Bld-HrTH - Madeira cockroach
C:Species: *Leucophaea madeira* (Madeira cockroach)
C:Date: 30-Jun-1992 #sequence_revision 14-Sep-1994 #text_change 24-Oct-1997
C:Accession: S08998
R:Gaede, G.; Rinehart, K.L.
Biol.Chem. Hoppe-Seyler 371, 345-354, 1990
A:Title: Primary structures of hypertrichalosemic neuropeptides isolated from the corpora enthalis and of the stick insect *Extatosoma tiaratum* assigned by tandem fast atom bombardment
A:Reference number: S08995; MUID:90253659; PMID:2340112
A:Accession: S08998
A:Molecule type: protein
A:Residues: 1-10 <GAB>
C:Superfamily: adipoikinetin hormone
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F:10/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 39.4%; Score 28; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 HYGPWM 11
::|||

DB 3 NFSPGM 8

RESULT 5
A26381
Hypertrichalosemic hormone - gray cockroach
C:Species: *Nauphoeta cinerea* (gray cockroach)
C:Date: 31-Mar-1998 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997
C:Accession: A26381
R:Gaede, G.; Rinehart, K.L.
Biochem. Biophys. Res. Commun. 141, 774-781, 1986
A:Title: Amino acid sequence of a hypertrichalosemic neuropeptide from the corpus carda
A:Reference number: A26381; MUID:87100208; PMID:3801028
A:Accession: A26381
A:Molecule type: protein
A:Residues: 1-10 <GAD>
A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C:Superfamily: adipoikinetin hormone
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F:10/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 39.4%; Score 28; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 HYGPWM 11
::|||

DB 3 NFSPGM 8

RESULT 6
S55310
adipoikinetin hormone - damselfly (*Pseudagrion inconnspicuum*)
N:Alternate names: Psi-AKH
C:Species: *Pseudagrion inconnspicuum*
C:Date: 19-Mar-1997 #sequence_revision 31-Oct-1997 #text_change 07-May-1999
C:Accession: S55310
R:Janssens, M.P.E.; Kellner, R.; Gaede, G.
Biochem. J. 302, 539-543, 1994
A:Title: A novel adipoikinetin octapeptide found in the damselflies *Pseudagrion inconnspicuum*
A:Reference number: S55310; MUID:94379987; PMID:8093008
A:Accession: S55310
A:Molecule type: protein
A:Residues: 1-8 <JAN>
C:Superfamily: adipoikinetin hormone
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F:10/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 36.6%; Score 26; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 HYGPWM 11
::|||

DB 3 NFSPGM 8

RESULT 7
A58620
adipoikinetin hormone - damselfly (*Ischnura senegalensis*)
C:Species: *Ischnura senegalensis*
C:Date: 28-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 07-May-1999
C:Accession: A58620
R:Janssens, M.P.E.; Kellner, R.; Gaede, G.
Biochem. J. 302, 539-543, 1994
A:Title: A novel adipoikinetin octapeptide found in the damselflies *Pseudagrion inconnspicuum*
A:Reference number: S55310; MUID:94379987; PMID:8093008
A:Accession: A58620
A:Molecule type: protein

A;Residues: 1-8 <JAN>
C;Superfamily: adipokinet hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 36.6%; Score 26; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.9e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 KHYGPGW 11
DB 3 NFTPGR 8

RESULT 8

gonadoliberin II - American alligator
N;Alternate names: gonadotropin-releasing hormone II
C;Species: Alligator mississippiensis (American alligator)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Mar-1997
C;Accession: B60066
R;Lovejoy, D.A.; Fischer, W.H.; Parker, D.B.; McRory, J.E.; Park, M.; Lance, V.; Swanson
Regul. Pept. 33, 105-116, 1991
A;Title: Primary structure of two forms of gonadotropin-releasing hormone from brains of
A;Reference number: A60066; MUID:91352338; PMID:1882082
A;Accession: B60066
A;Molecule type: protein
A;Residues: 1-10 <LOV>

C;Superfamily: gonadoliberin
C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 36.6%; Score 26; DB 1; Length 10;
Best Local Similarity 42.9%; Pred. No. 2.9e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 KHYGPGW 11
DB 1 QHNSHGW 7

RESULT 9

A61126
gonadoliberin - spotted ratfish
N;Alternate names: gonadotropin-releasing hormone
C;Species: Hydrotaea collieri (spotted ratfish)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 18-Mar-1997
C;Accession: A61126
R;Lovejoy, D.A.; Sherwood, N.M.; Fischer, W.H.; Jackson, B.C.; Rivier, J.E.; Lee, T.
Gen. Comp. Endocrinol. 82, 152-161, 1991
A;Title: Primary structure of gonadotropin-releasing hormone from the brain of a holocarp
A;Reference number: A61126; MUID:91340067; PMID:1678723
A;Accession: A61126
A;Molecule type: protein
A;Residues: 1-10 <LOV>

A;Experimental source: brain
C;Superfamily: gonadoliberin
C;Keywords: amidated carboxyl end; brain; hormone; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 36.6%; Score 26; DB 1; Length 10;
Best Local Similarity 42.9%; Pred. No. 2.9e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 KHYGPGW 11
DB 1 QHNSHGW 7

RESULT 10

B46030

gonadoliberin II - spiny dogfish
N;Alternate names: gonadotropin-releasing hormone
C;Species: Squalus acanthias (spiny dogfish)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jan-2003
C;Accession: B46030
R;Lovejoy, D.A.; Fischer, W.H.; Ngamwongchon, S.; Craig, A.G.; Nahorniak, C.S.; Peter, R.
Proc. Natl. Acad. Sci. U.S.A. 89, 6373-6377, 1992
A;Title: Distinct sequence of gonadotropin-releasing hormone (GNRH) in dogfish brain pro
A;Reference number: A46030; MUID:92335300; PMID:1631133
A;Accession: B46030
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <LOV>

C;Superfamily: gonadoliberin
C;Keywords: hormone; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 36.6%; Score 26; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 2.9e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 KHYGPGW 11
DB 1 QHNSHGW 7

RESULT 11

A46030
gonadoliberin I - spiny dogfish
N;Alternate names: gonadotropin-releasing hormone
C;Species: Squalus acanthias (spiny dogfish)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Dec-1998
C;Accession: A46030
R;Lovejoy, D.A.; Fischer, W.H.; Ngamwongchon, S.; Craig, A.G.; Nahorniak, C.S.; Peter, R.
Proc. Natl. Acad. Sci. U.S.A. 89, 6373-6377, 1992
A;Title: Distinct sequence of gonadotropin-releasing hormone (GNRH) in dogfish brain pro
A;Reference number: A46030; MUID:92335300; PMID:1631133
A;Accession: A46030
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <LOV>

C;Keywords: hormone; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 36.6%; Score 26; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 2.9e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 KHYGPGW 11
DB 1 QHNSHGW 7

RESULT 12

S15422
adipokinet hormone - cockchafer
C;Species: Melolontha melolontha (cockchafer)
C;Date: 19-Mar-1997 #sequence_revision 31-Oct-1997 #text_change 31-Oct-1997
C;Accession: S15422
R;Gaede, G.
Biochem. J. 275, 671-677, 1991
A;Title: A unique charged tyrosine-containing member of the adipokinet hormone/red-p
A;Reference number: S15422; MUID:91248100; PMID:2039445
A;Accession: S15422
A;Molecule type: protein
A;Residues: 1-8 <BIO>

C;Superfamily: adipokinet hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 35.2%; Score 25; DB 2; Length 8;

Thu Sep 2 07:41:39 2004

Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 HYGPGW 11
: |||
Db 3 NYSFDM 8

RESULT 13

A33995

adipokinetin hormone - black horse fly

C/Species: Tabanus atratus (black horse fly)

C/Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 31-Oct-1997

C/Accession: A33995

R/Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhang,

Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989

A/Title: Primary structure of two neuropeptide hormones with adipokinetin and hypocretinal

A/Reference number: A33995; PMID:90046758; PMID:2813385

A/Accession: A33995

A/Molecule type: protein

A/Residues: 1-8 <JAF>

C/Superfamily: adipokinetin hormone

C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted

F/8/Modified site: amidated carboxyl end (Trp) #status predicted

Query Match 35.2%; Score 25; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 14

A58641

adipokinetin hormone - dor beetle

C/Species: Geotrupes stercorarius (dor beetle)

C/Date: 28-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 31-Oct-1997

C/Accession: A58641

R/Gaede, G.

Biochem. J. 275, 671-677, 1991

A/Title: A unique charged tyrosine-containing member of the adipokinetin hormone/red-pi

A/Reference number: S15422; PMID:91248100; PMID:2033445

A/Accession: A58641

A/Molecule type: protein

A/Residues: 1-8 <BIO>

C/Superfamily: adipokinetin hormone

C/Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F/8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 35.2%; Score 25; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 15

S21663

neuropeptide - flower beetle (Pachnoda marginata)

C/Species: Pachnoda marginata

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997

C/Accession: S21663

R/Gaede, G.; Lohpata, A.; Kellner, R.; Rinehart, K.L.

Biochem. Chem. Hoppe-Seyler 373, 133-142, 1992

A/Title: Primary structures of neuropeptides isolated from the corpora cardiaca of vari

A/Reference number: S21663; PMID:92265187; PMID:1586453

A/Accession: S21663
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-8 <GAE>

Query Match 35.2%; Score 25; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 HYGPGW 11
: |||
Db 3 NYSFDM 8

RESULT 16

B33995

hypocretalin hormone - black horse fly

C/Species: Tabanus atratus (black horse fly)

C/Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 31-Oct-1997

C/Accession: B33995

R/Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhang,

Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989

A/Title: Primary structure of two neuropeptide hormones with adipokinetin and hypocretalin

A/Reference number: A33995; PMID:90046758; PMID:2813385

A/Accession: B33995

A/Molecule type: protein

A/Residues: 1-10 <JAF>

C/Superfamily: adipokinetin hormone

C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted

F/10/Modified site: amidated carboxyl end (Tyr) #status predicted

Query Match 35.2%; Score 25; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 YGPGW 11
: |||
Db 4 FTPGW 8

RESULT 17

A21114

gonadoliberin - chum salmon

C/Species: Oncorhynchus keta (chum salmon)

C/Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 18-Jun-1993

C/Accession: A21114

R/Sherwood, N.; Elden, L.; Brownstein, M.; Spiess, J.; Rivier, J.; Vale, W.

Proc. Natl. Acad. Sci. U.S.A. 80, 2794-2798, 1983

A/Title: Characterization of a teleost gonadotropin-releasing hormone.

A/Reference number: A21114; PMID:83195140; PMID:6341999

A/Accession: A21114

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-10 <SHE>

RESULT 18

S39030

lyeyl-bradykinin - rainbow trout

C/Species: Oncorhynchus mykiss (rainbow trout)

C/Date: 19-May-1994 #sequence_revision 19-Apr-1996 #text_change 18-Aug-2000

C/Accession: S39030

R/Conlon, J.M.; Olson, K.R.

FEBS Lett. 334, 75-78, 1993

A>Title: Purification of a vasoactive peptide related to lysyl-bradykinin from trout pla
A/Reference number: S39030; MUID:94039817; PMID:8224232
A/Accession: S39030
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-10 <CON>
C/Superfamily: unassigned animal peptides

Query Match 33.8%; Score 24; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGM 11
|||
Db 4 PGM 6

RESULT 19
S70338
napin small chain S3A - Swedish turnip (fragment)
C/Species: Brassica napus var. rapifera (Swedish turnip, rutabaga)
C/Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
C/Accession: S70338
R/Neumann, G.M.; Condron, R.; Thomas, I.; Polya, G.M.
Biochim. Biophys. Acta 1295, 23-33, 1996
A>Title: Purification and sequencing of multiple forms of Brassica napus seed napin sma
A/Reference number: S70336; MUID:96283790; PMID:8679670
A/Accession: S70338
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-11 <NEU>

Query Match 33.8%; Score 24; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 6.9e+02;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 GPGW 11
|||
Db 8 GPSW 11

RESULT 20
PH1322
Ig heavy chain DJ region (clone C344-99) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C/Accession: PH1322
R/Wasserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A>Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A/Reference number: PH1302; MUID:93034761; PMID:1460419
A/Accession: PH1322
A/Molecule type: DNA
A/Residues: 1-14 <WAS>
C/Keywords: heterotetramer; immunoglobulin

Query Match 33.8%; Score 24; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 8.8e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 YGPGW 11
|||
Db 2 WSGGW 6

RESULT 21
PT0288
Ig heavy chain CRD3 region (clone 4-106) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C/Accession: PT0288
R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Calton, A.U.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991

A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and Jc
A/Reference number: PT0222; MUID:91108357; PMID:1899102
A/Accession: PT0288
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-9 <YAM>
A/Experimental source: B lymphocyte
C/Keywords: heterotetramer; immunoglobulin

Query Match 32.4%; Score 23; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 YGPGW 11
|||
Db 5 YSSGW 9

RESULT 22
S65388
cytochrome-c oxidase (EC 1.9.3.1) chain VII c, hepatic - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C/Accession: S65388; S65389
R/Schaeffer, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.
Eur. J. Biochem. 230, 235-241, 1995
A>Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term
A/Reference number: S65372; MUID:95324529; PMID:7601105
A/Accession: S65388
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-10 <SCH>
A/Accession: S65389
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-10 <SC2>
C/Superfamily: cytochrome-c oxidase chain VIIc
C/Keywords: oxidoreductase

Query Match 32.4%; Score 23; DB 2; Length 10;
Best Local Similarity 71.4%; Pred. No. 9.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 6 HY--GPG 10
|||
Db 2 HYEGPG 8

RESULT 23
S77990
cytochrome-c oxidase (EC 1.9.3.1) chain VIIC - bigeye tuna (fragment)
C/Species: Thunnus obesus (bigeye tuna)
C/Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 30-Jan-1998
C/Accession: S77990
R/Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lotzspich, F.; Kadenbach, B.
Submitted to the Protein Sequence Database, June 1997
A/Reference number: S77980
A/Accession: S77990
A/Molecule type: protein
A/Residues: 1-10 <ARN>
A/Experimental source: heart; liver
C/Genetics: nuclear
A/Genome: nuclear
C/Function: oxidative phosphorylation; respiratory chain
A/Pathway: electron transfer; membrane-associated complex; mitochondrial inner membrane
C/Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 32.4%; Score 23; DB 2; Length 10;
Best Local Similarity 71.4%; Pred. No. 9.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 6 HY--GPG 10
|||
Db 2 HYEGPG 8

RESULT 24

PT0302
Ig heavy chain CDR3 region (clone 5-112) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C/Accession: PT0302
R/Yamada, M.; Massemann, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
U. Exp. Med. 173, 395-407, 1991
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A/Reference number: PT0222; MUID:91108337; PMID:189102
A/Accession: PT0302
A/Molecule type: DNA
A/Residues: 1-11 <YAM>
A/Experimental source: B lymphocyte
C/Keywords: heterotrimer; immunoglobulin

Query Match

Best Local Similarity 32.4%; Score 23; DB 2; Length 11;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 YGPGW 11
DB 6 YSSGW 10

RESULT 25

S08995
hypertrihaloemic hormone I - oriental cockroach
M/Alternate names: Pea-CAH-I
C/Species: Blatta orientalis (oriental cockroach)
C/Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997
C/Accession: S08995
R/Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A/Title: Primary structures of hypertrihaloemic neuropeptides isolated from the corpora
aenalis and of the stick insect *Extatosoma tiaratum* assigned by tandem fast atom bombard
A/Reference number: S08995; MUID:90253659; PMID:2340112
A/Accession: S08995
A/Molecule type: protein
A/Residues: 1-8 <GAE>
A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C/Superfamily: adipokinetic hormone
C/Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F/8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match

Best Local Similarity 31.0%; Score 22; DB 2; Length 8;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 HYGPWM 11
DB 3 NFSPWM 8

RESULT 26

A49823
adipokinetic hormone I - American cockroach
M/Alternate names: periplaneta CC-1
C/Species: Periplaneta americana (American cockroach)
C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
C/Accession: A49823
R/Scarborough, R.W.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEnroe, G.A.; Miller, C.
Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984
A/Title: Isolation and primary structure of two peptides with cardioacceleratory and hyp
A/Reference number: A49823; MUID:84298179; PMID:6591205
A/Accession: A49823
A/Molecule type: protein
A/Residues: 1-8 <SCA>
C/Superfamily: adipokinetic hormone
C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F/8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match

Best Local Similarity 31.0%; Score 22; DB 2; Length 8;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 HYGPWM 11
DB 3 NFSPWM 8

RESULT 27

A44960
neuropeptide Ied-CC-I - Colorado potato beetle
C/Species: Leptinotarsa decemlineata (Colorado potato beetle)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C/Accession: A44960
R/Gaede, G.; Kellner, R.
Peptides 10, 1287-1289, 1989
A/Title: The metabolic neuropeptides of the corpus cardiaca from the potato beetle and
A/Reference number: A44960; MUID:90160053; PMID:2576128
A/Accession: A44960
A/Molecule type: protein
A/Residues: 1-8 <GAE>
C/Superfamily: adipokinetic hormone
C/Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F/8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimental

Query Match

Best Local Similarity 31.0%; Score 22; DB 2; Length 8;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 HYGPWM 11
DB 3 NFSPWM 8

RESULT 28

A43976
hypertrihaloemic hormone - yellow mealworm
C/Species: Tenebrio molitor (yellow mealworm)
C/Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 07-May-1999
C/Accession: A43976
R/Gaede, G.; Rosinski, G.
Peptides 11, 455-459, 1990
A/Title: The primary structure of the hypertrihaloemic neuropeptide from tenebrionid bee
A/Reference number: A43976; MUID:90341081; PMID:2381871
A/Accession: A43976
A/Molecule type: protein
A/Residues: 1-8 <GAE>
C/Superfamily: adipokinetic hormone
C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F/8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match

Best Local Similarity 31.0%; Score 22; DB 2; Length 8;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 HYGPWM 11
DB 3 NFSPWM 8

RESULT 29

B43976
hypertrihaloemic hormone - beetle (*Zophobas rugipes*)
C/Species: Zophobas rugipes
C/Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 07-May-1999
C/Accession: B43976
R/Gaede, G.; Rosinski, G.

Peptides 11, 455-459, 1990
 A:Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid be
 A:Reference number: A43976; PMID:90341081; PMID:2381871
 A:Accession: B43976
 A:Molecule type: protein
 A:Residues: 1-8 <GAB>
 C:Superfamily: adipoiknetic hormone
 C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
 F.11/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F.13/Modified site: amidated carboxyl end (Tyr) #status experimental

Query Match 31.0%; Score 22; DB 2; Length 8;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 HYGPGW 11
 DB 3 NPSPMW 8

RESULT 30
 A05169
 neuropeptide M-1 - American cockroach
 C:Species: Periplaneta americana (American cockroach)
 C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Dec-1993
 C:Accession: A05169
 R:Witten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.L.
 Biochem. Biophys. Res. Commun. 124, 350-358, 1984
 A:Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mas
 A:Reference number: A90118; PMID:85046530; PMID:6546628
 A:Accession: A05169
 A:Molecule type: protein
 A:Residues: 1-8 <MTT>
 C:Keywords: neuropeptide

Query Match 31.0%; Score 22; DB 2; Length 8;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 HYGPGW 11
 DB 3 NPSPMW 8

RESULT 31
 RHLMGS
 gonadoliberin - sea lamprey
 N:Alternate names: gonadotropin releasing hormone (GNRH)
 C:Species: Petromyzon marinus (sea lamprey)
 C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 18-Mar-1997
 C:Accession: A01412
 R:Sherwood, N.M.; Sower, S.A.; Marshak, D.R.; Fraser, B.A.; Brownstein, M.J.
 J. Biol. Chem. 261, 4812-4819, 1986
 A:Title: Primary structure of gonadotropin-releasing hormone from lamprey brain.
 A:Reference number: A01412; PMID:86168192; PMID:3514603
 A:Accession: A01412
 A:Molecule type: protein
 A:Residues: 1-10 <SHE>
 C:Comment: This hormone was isolated from the brain.
 C:Superfamily: gonadoliberin
 C:Keywords: amidated carboxyl end; hormone; pyroglutamic acid
 F.11/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F.13/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 31.0%; Score 22; DB 1; Length 10;
 Best Local Similarity 42.9%; Pred. No. 1.4e+03;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 KHGPGW 11
 DB 1 QHYSLEW 7

RESULT 32
 S53789
 neuropeptide Pec-HrTH - Platypleura capensis
 C:Species: Platypleura capensis
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
 C:Accession: S53789
 R:Gaede, G.; Janssens, M.P.E.
 Biol. Chem. Hoppe-Seyler 375, 803-809, 1994
 A:Title: Cicadas contain novel members of the AKH/RPCH family peptides with hypertrehalo
 A:Reference number: S53789; PMID:95225985; PMID:7710694
 A:Accession: S53789
 A:Molecule type: protein
 A:Residues: 1-10 <GAB>
 C:Keywords: blocked amino end; blocked carboxyl end

Query Match 31.0%; Score 22; DB 2; Length 10;
 Best Local Similarity 33.3%; Pred. No. 1.4e+03;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 HYGPGW 11
 DB 3 NPSPMW 8

RESULT 33
 S05002
 corazonin - American cockroach
 C:Species: Periplaneta americana (American cockroach)
 C:Date: 07-Sep-1990 #sequence_revision 09-Apr-1998 #text_change 09-Apr-1998
 C:Accession: S05002
 R:Veensstra, J.A.
 FEBS Lett. 250, 231-234, 1989
 A:Title: Isolation and structure of corazonin, a cardioactive peptide from the american
 A:Reference number: S05002; PMID:89325572; PMID:2753132
 A:Accession: S05002
 A:Molecule type: protein
 A:Residues: 1-11 <VES>
 C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
 F.11/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F.13/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 31.0%; Score 22; DB 2; Length 11;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 YGPGW 11
 DB 5 YSRGW 9

RESULT 34
 A60409
 bombesin-like peptide L - frog (Pseudophryne guentheri)
 C:Species: Pseudophryne guentheri
 C:Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 18-Aug-2000
 C:Accession: A60409
 R:Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
 Peptides 11, 299-304, 1990
 A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austro
 A:Reference number: A60409; PMID:90287814; PMID:2356157
 A:Accession: A60409
 A:Molecule type: protein
 A:Residues: 1-13 <STV>
 C:Superfamily: unassigned animal peptides
 C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
 F.11/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F.13/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 31.0%; Score 22; DB 2; Length 13;
 Best Local Similarity 75.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 GPGW 11

Db 4 GPOW 7

RESULT 35

S23640

Ig kappa chain J segment (J-kappa-3) - human

C/Species: Homo sapiens (man)

C/Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996

C/Accession: S23640

R/Huber, C.; Klobeck, H.G.; Zachau, H.G.

Eur. J. Immunol. 22, 1561-1565, 1992

A/Title: Ongoing V(kappa)-J(kappa) recombination after formation of a productive V(kappa)

A/Reference number: S23637; MUID:92289816; PMID:1601042

A/Accession: S23640

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-13 <HUB>

A/Cross-references: EMBL:X63370

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1991

C/Keywords: heterotrimer; immunoglobulin

Query Match 31.0%; Score 22; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 YGPG 10
|||
Db 3 FGPG 6

RESULT 36

S33802

Chaperone, TCPI-related - cat

C/Species: Avena sativa (oat)

C/Date: 02-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 17-Mar-1999

C/Accession: S33802

R/Nummert, E.; Grimm, R.; Speith, V.; Eckerstrom, C.; Schiltz, E.; Gatenby, A.A.; Schaefer

Nature 363, 644-648, 1993

A/Title: A TCPI-related molecular chaperone from plants refolds phytochrome to its photo

A/Reference number: S33800; MUID:93288140; PMID:8093715

A/Accession: S33802

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-14 <MTM>

Query Match 31.0%; Score 22; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 GPGW 11
|||
Db 8 GPMW 11

RESULT 37

PT0209

T-cell receptor alpha chain V-J region (4-1-L.6) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997

C/Accession: PT0209

R/Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A/Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted

A/Reference number: PT0209; MUID:91217621; PMID:1902501

A/Accession: PT0209

A/Molecule type: mRNA

A/Residues: 1-11 <NAK>

C/Keywords: T-cell receptor

Query Match 29.6%; Score 21; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HYG 8
|||
Db 6 HYG 8

RESULT 38

PH1593

Ig H chain V-D-J region (wild-type clone 144) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C/Accession: PH1593

R/Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A/Title: Molecular characterization of transgene-induced immunodeficiency in B-1ess mice

A/Reference number: PH1580; MUID:93301609; PMID:8315387

A/Accession: PH1593

A/Molecule type: DNA

A/Residues: 1-13 <LEV>

A/Experimental source: bone marrow pre-B lymphocyte

C/Keywords: immunoglobulin

Query Match 29.6%; Score 21; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LKHY 7
|||
Db 5 LRHY 8

RESULT 39

S03530

Ig heavy chain J region (JH-4) - African clawed frog

C/Species: Xenopus laevis (African clawed frog)

C/Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 21-Jul-2000

C/Accession: S03530

R/Schwager, J.; Grossberger, D.; du Pasquier, L.

EMBO J. 7, 2409-2415, 1988

A/Title: Organization and rearrangement of immunoglobulin M genes in the amphibian Xenopus

A/Reference number: S01158; MUID:89052653; PMID:2903824

A/Accession: S03530

A/Molecule type: DNA

A/Residues: 1-14 <SCH>

Query Match 29.6%; Score 21; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 HYG 10
|||
Db 3 HMG 7

RESULT 40

A28004

adipokinetin hormone G - two-spotted cricket

N/Alternate names: AKH-G

C/Species: Gryllus bimaculatus (two-spotted cricket)

C/Date: 30-Jun-1989 #sequence_revision 24-Oct-1997 #text_change 24-Oct-1997

C/Accession: A28004

R/Gaede, G.; Rinehart, K.L.

Biochem. Biophys. Res. Commun. 149, 908-914, 1987

A/Title: Primary sequence analysis by fast atom bombardment mass spectrometry of a peptide

A/Reference number: A28004; MUID:88106553; PMID:3426616

A/Accession: A28004

A/Molecule type: protein

A/Residues: 1-8 <GAE>

A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have

C/Superfamily: adipokinetin hormone

C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F./Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F/8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 28.2%; Score 20; DB 2; Length 8;

Best Local Similarity 33.3%; Pred. No. 2.8e+05;

Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 HYPGW 11

DB 3 NPTPSW 8

RESULT 41

S10596 adipokinetic hormone - pond skimmer

C:Species: Libellula auripennis

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 14-Nov-1997

C:Accession: S10596

R:Gaede, G.

Biol. Chem. Hoppe-Seyler 371, 475-483, 1990

A:Title: The putative ancestral peptide of the adipokinetic/red-pigment-concentrating ho

A:Reference number: S10596; MUID:90359055; PMID:2390213

A:Accession: S10596

A:Molecule type: protein

A:Residues: 1-8 <BIO>

C:Comment: This peptide has both adipokinetic and hypertrehalosemic activities.

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F/8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 28.2%; Score 20; DB 2; Length 8;

Best Local Similarity 33.3%; Pred. No. 2.8e+05;

Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 HYPGW 11

DB 3 NPTPSW 8

RESULT 42

S11545 adipokinetic hormone - nestling-sucking blowfly

C:Species: Protophormia terraenovae (nestling-sucking blowfly)

C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 31-Oct-1997

C:Accession: S11545

R:Gaede, G.; Wilps, H.; Kellner, R.

Biochem. J. 269, 309-313, 1990

A:Title: Isolation and structure of a novel charged member of the red-pigment-concentrat

extraenovae (Diptera).

A:Reference number: S11545; MUID:90351345; PMID:2386478

A:Accession: S11545

A:Molecule type: protein

A:Residues: 1-8 <GAB>

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F/8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 28.2%; Score 20; DB 2; Length 8;

Best Local Similarity 40.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 YGPGW 11

DB 4 FSPDW 8

RESULT 43

PT0368

Ig gamma chain C region (gamma-1) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Aug-1996

C:Accession: PT0368

R.Millil, M.; Fougereau, M.; Guglielmi, P.; Schiff, C.

Mol. Immunol. 28, 753-761, 1991

A:Title: Early occurrence of immunoglobulin isotype switching in human fetal liver.

A:Reference number: PT0368; MUID:91312348; PMID:1906981

A:Accession: PT0368

A:Molecule type: mRNA

A:Residues: 1-8 <MIL>

A:Experimental source: fetal liver

C:Keywords: immunoglobulin

Query Match 28.2%; Score 20; DB 2; Length 8;

Best Local Similarity 75.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 HYPG 9

DB 2 HQGP 5

RESULT 44

P00786 NADH2 dehydrogenase (EC 1.6.99.3) 26k chain - fava bean mitochondrion (fragment)

N:Alternate names: complex I 26k chain; NADH-ubiquinone reductase 26k chain

C:Species: mitochondrion Vicia faba (fava bean)

C>Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 03-Jun-2002

C:Accession: P00786

R:Leberme, S.; Baulty, M.

Plant Physiol. 102, 435-443, 1993

A:Title: Purification and preliminary characterization of mitochondrial complex I (NADH:

A:Reference number: P00785; MUID:94151437; PMID:8108509

A:Accession: P00786

A:Molecule type: protein

A:Residues: 1-12 <LET>

C:Comment: Complex I, mitochondrial NADH-ubiquinone reductase, is the first of the th

transferring from 5K to 75K.

C:Comment: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinone by

A:Genome: mitochondrion

C:Keywords: electron transfer; mitochondrion; oxidoreductase

Query Match 28.2%; Score 20; DB 2; Length 12;

Best Local Similarity 75.0%; Pred. No. 3.6e+03;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 YGPG 10

DB 8 YAPG 11

RESULT 45

P00152 18K iron-sulfur protein - Chlamydomonas reinhardtii chloroplast (fragment)

N:Alternate names: frxB homolog

C:Species: chloroplast Chlamydomonas reinhardtii

C>Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 30-Sep-1993

C:Accession: P00152

R:Wu, M.; Nle, Z.Q.; Yang, J.

Plant Cell 1, 551-557, 1989

A:Title: The 18-KD protein that binds to the chloroplast DNA replicative origin is an ir

A:Reference number: P00152; MUID:92404720; PMID:2562513

A:Accession: P00152

A:Molecule type: protein

A:Residues: 1-14 <WDM>

C:Genetics:

A:Genome: chloroplast

C:Keywords: chloroplast

Query Match 28.2%; Score 20; DB 2; Length 14;

Best Local Similarity 50.0%; Pred. No. 4.2e+03;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 KXHYG 9

DB 3 KXHYG 9

Thu Sep 2 07:41:39 2004

us-09-720-469a-5.aug30.rpr

Page 10

Db 7 BFKNYG 12

Search completed: August 30, 2004, 10:58:50
Job time : 4.30743 secs

Thu Sep 2 07:41:38 2004

us-09-720-469a-5.aug30.rapb

Page 1

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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:49:45 ; Search time 13.4527 Seconds

(without alignments)
257.253 Million cell updates/sec

Title: US-09-720-469a-5

Perfect score: 71

Sequence: 1 NFKLHYGPGW 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues 149443

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 8

Maximum DB seq length: 14

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	45	63.4	14	US-10-394-980-52	Sequence 52, Appl
2	36	50.7	13	US-10-038-612-168	Sequence 168, Appl
3	31	43.7	8	US-09-849-092-2	Sequence 2, Appl
4	31	43.7	11	US-09-791-551-99	Sequence 99, Appl
5	30	42.3	8	US-09-880-748-2870	Sequence 2870, Appl
6	30	42.3	11	US-10-293-418-2870	Sequence 2870, Appl
7	30	42.3	11	US-10-169-710-23	Sequence 23, Appl
8	30	42.3	13	US-10-038-612-168	Sequence 168, Appl
9	30	42.3	13	US-10-239-321A-52	Sequence 52, Appl
10	29	40.8	10	US-10-450-036A-95	Sequence 95, Appl
11	28	39.4	8	US-09-910-552-37	Sequence 37, Appl
12	28	39.4	8	US-10-643-465-37	Sequence 37, Appl
13	28	39.4	10	US-10-072-419-2	Sequence 2, Appl
14	27	38.0	9	US-10-013-312-41	Sequence 41, Appl
15	27	38.0	9	US-10-013-312-235	Sequence 235, Appl

16	27	38.0	9	US-10-013-312-512	Sequence 512, Appl
17	27	38.0	9	US-10-013-312-602	Sequence 602, Appl
18	27	38.0	9	US-10-013-312-1404	Sequence 1404, Appl
19	27	38.0	9	US-10-013-312-1464	Sequence 1464, Appl
20	27	38.0	9	US-10-013-312-1554	Sequence 1554, Appl
21	27	38.0	9	US-10-013-312-1612	Sequence 1612, Appl
22	27	38.0	9	US-10-013-312-1672	Sequence 1672, Appl
23	27	38.0	9	US-10-013-312-1976	Sequence 1976, Appl
24	27	38.0	10	US-10-013-312-52	Sequence 52, Appl
25	27	38.0	10	US-10-013-312-183	Sequence 183, Appl
26	27	38.0	10	US-10-013-312-254	Sequence 254, Appl
27	27	38.0	10	US-10-013-312-384	Sequence 384, Appl
28	27	38.0	10	US-10-013-312-497	Sequence 497, Appl
29	27	38.0	10	US-10-013-312-664	Sequence 664, Appl
30	27	38.0	10	US-10-013-312-686	Sequence 686, Appl
31	27	38.0	10	US-10-013-312-2094	Sequence 2094, Appl
32	27	38.0	10	US-10-013-312-2114	Sequence 2114, Appl
33	27	38.0	10	US-10-013-312-2217	Sequence 2217, Appl
34	27	38.0	10	US-10-013-312-2250	Sequence 2250, Appl
35	27	38.0	10	US-10-013-312-2321	Sequence 2321, Appl
36	27	38.0	10	US-10-013-312-2339	Sequence 2339, Appl
37	27	38.0	10	US-10-013-312-2407	Sequence 2407, Appl
38	27	38.0	10	US-10-360-101-155	Sequence 155, Appl
39	27	38.0	10	US-10-360-101-156	Sequence 156, Appl
40	27	38.0	10	US-10-360-101-157	Sequence 157, Appl
41	27	38.0	10	US-10-723-434-113	Sequence 113, Appl
42	27	38.0	10	US-10-723-434-112	Sequence 112, Appl
43	27	38.0	12	US-10-286-457-132	Sequence 132, Appl
44	26	36.6	8	US-10-182-252A-200	Sequence 200, Appl
45	26	36.6	14	US-10-062-710-162	Sequence 162, Appl

ALIGNMENTS

RESULT 1

US-10-394-980-52

Sequence 52, Application US/10394980

Publication No. US20040005633A1

GENERAL INFORMATION:

APPLICANT: VandeKerkhove, Joel

APPLICANT: Gevaert, Kris

TITLE OF INVENTION: METHODS AND APPARATUS FOR GEL-FREE QUALITATIVE AND

FILE REFERENCE: VAV-001

CURRENT FILING DATE: 2003-03-21

PRIOR FILING DATE: 2002-03-22

PRIOR APPLICATION NUMBER: US60/278,171

PRIOR FILING DATE: 2001-03-22

PRIOR APPLICATION NUMBER: US60/318,749

PRIOR FILING DATE: 2001-09-12

PRIOR APPLICATION NUMBER: US60/323,999

NUMBER OF SEQ ID NOS: 473

SOFTWARE: PatentIn version 3.1

SEQ ID NO 52

LENGTH: 14

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: MISC FEATURE

OTHER INFORMATION: Part of CYP2_HUMAN (peptidyl-prolyl cis-trans isomerase B)

US-10-394-980-52

Query Match

Beat Local Similarity 63.4%; Score 45; DB 15; Length 14;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

HYGPGW 11

1 HYGPGW 6

DB

RESULT 2
US-10-038-612-168
Sequence 168, Application US/10038612
Publication No. US20020160478A1
GENERAL INFORMATION:
APPLICANT: Ben-Sasson, Shmuel A.
TITLE OF INVENTION: Short Peptides Which Selectively
Modulate the Activity of Protein Kinases
FILE REFERENCE: 1242.1029-000 (CMCC-679)
CURRENT APPLICATION NUMBER: US/10/038,612
CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 09/161,094
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 172
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 168
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MYRISTATE
LOCATION: (1)...(0)
NAME/KEY: AMIDATION
LOCATION: (0)...(13)
OTHER INFORMATION: TrkB
US-10-038-612-168

Query Match
Best Local Similarity 50.7%; Score 36; DB 13; Length 13;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NFKLKHGP 9
DB 3 NFKLRAHGP 11

RESULT 3
US-09-849-092-2
Sequence 2, Application US/09849092
Publication No. US20030032169A1
GENERAL INFORMATION:
APPLICANT: Eriksson, Ulf; Simon, Andreas; Romert, Anna
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE WHICH
CODES FOR A 32 KDA PROTEIN HAVING 11-CIS RETINOL DEHYDROGENASE
TITLE OF INVENTION: ACTIVITY AND WHICH ASSOCIATES WITH P63, A PORTION OF A
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/849,092
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/729,594
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/375,962
FILING DATE: 20-January-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/258,418
FILING DATE: 10-June-1994

ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. US20030032169A1man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5372.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-849-092-2

Query Match
Best Local Similarity 43.7%; Score 31; DB 10; Length 8;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 YGPGM 11
DB 1 YSPGM 5

RESULT 4
US-09-791-551-99
Sequence 99, Application US/09791551
Publication No. US20030235864A1
GENERAL INFORMATION:
APPLICANT: KLOETZER, WILLIAM S.
TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES
FILE REFERENCE: 037003/0277869
CURRENT APPLICATION NUMBER: US/09/791,551
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 60/185,390
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: 60/233,625
PRIOR FILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 119
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 99
LENGTH: 11
TYPE: PRT
ORGANISM: Mus sp.
US-09-791-551-99

Query Match
Best Local Similarity 43.7%; Score 31; DB 11; Length 11;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 HYGPM 11
DB 2 HYGSM 7

RESULT 5
US-09-880-748-2870
Sequence 2870, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Bly5
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 2870
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-2870

Query Match 42.3%; Score 30; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GPGW 11
DB 2 GPGW 5

RESULT 6
US-10-293-418-2870
Sequence 2870, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Bly5
FILE REFERENCE: PFS23P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO: 2870
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-2870

Query Match 42.3%; Score 30; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GPGW 11
DB 2 GPGW 5

RESULT 7
US-10-169-710-23
Sequence 23, Application US/10169710
Publication No. US20030181362A1
GENERAL INFORMATION:
APPLICANT: INNOGENETICS
TITLE OF INVENTION: HUMAN AND PARASITE ORPHAN RECEPTOR PROTEINS
FILE REFERENCE: 2551-79
CURRENT APPLICATION NUMBER: US/10/169,710
CURRENT FILING DATE: 2002-07-09
PRIOR APPLICATION NUMBER: PCT/GB01/00085

PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: GB0000474.7
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 23
LENGTH: 11
TYPE: PRT
ORGANISM: Shistosoma haematobium
US-10-169-710-23

Query Match 42.3%; Score 30; DB 14; Length 11;
Best Local Similarity 57.1%; Pred. No. 3.5e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 KLRHGP 9
DB 4 KLRHGP 10

RESULT 8
US-10-038-612-169
Sequence 169, Application US/10038612
Publication No. US20020160478A1
GENERAL INFORMATION:
APPLICANT: Ben-Sasson, Shmuel A.
TITLE OF INVENTION: Short peptides which selectively
inhibit the activity of protein kinases
FILE REFERENCE: 1242.1029-000 (CMCC-679)
CURRENT APPLICATION NUMBER: US/10/038,612
CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 09/161,094
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 172
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 169
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
NAME/KEY: MYRISTATE
LOCATION: (1)...(0)
NAME/KEY: AMIDATION
LOCATION: (0)...(13)
OTHER INFORMATION: TRYK
US-10-038-612-169

Query Match 42.3%; Score 30; DB 13; Length 13;
Best Local Similarity 62.5%; Pred. No. 4.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FKLKRG 9
DB 2 FKLKRG 9

RESULT 9
US-10-239-321A-52
Sequence 52, Application US/10239321A
Publication No. US20040116336A1
GENERAL INFORMATION:
APPLICANT: KITADA, Chieko
APPLICANT: NISHIZAWA, Naoki
APPLICANT: HINUMA, Shuji
APPLICANT: HOSODA, Masaki
TITLE OF INVENTION: Peptide derivative
FILE REFERENCE: 2702 USOP
CURRENT APPLICATION NUMBER: US/10/239,321A
CURRENT FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: PCT/JP01/02278
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: JP 12-87114
PRIOR FILING DATE: 2000-03-23

;; PRIOR APPLICATION NUMBER: JP 12-288891
;; PRIOR FILING DATE: 2000-09-19
;; NUMBER OF SEQ ID NOS: 72
;; SEQ ID NO 52
;; LENGTH: 13
;; TYPE: PRT
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: peptide derivative
;; NAME/KEY: MISC FEATURE
;; LOCATION: (1)..(1)
;; OTHER INFORMATION: Xaa means pglu
US-10-239-321A-52

Query Match
Best Local Similarity 42.3%; Score 30; DB 16; Length 13;
Best Local Similarity 57.1%; Pred. No. 4.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 KLKHYGP 9
Db 4 RLSHFGP 10

RESULT 10
US-10-450-036A-95
;; Sequence 95, Application US/10450036A
;; Publication No. US20040161738A1
;; GENERAL INFORMATION:
;; APPLICANT: MTRUGANANDAM, ARUMUGAM
;; APPLICANT: TANHA, JASWID
;; APPLICANT: NARANG, SARAM
;; APPLICANT: STANIMIROVIC, DANICA
;; TITLE OF INVENTION: SINGLE-DOVAIN BRAIN TARGETING ANTIBODY FRAGMENTS
;; TITLE OF INVENTION: DERIVED FROM LLAMA ANTIBODIES
;; FILE REFERENCE: 1339-25
;; CURRENT APPLICATION NUMBER: US/10/450,036A
;; CURRENT FILING DATE: 2004-01-09
;; PRIOR APPLICATION NUMBER: PCT/CA01/00783
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: US 60/263,108
;; PRIOR FILING DATE: 2001-01-22
;; NUMBER OF SEQ ID NOS: 101
;; SOFTWARE: PatentIn Ver. 3.2
;; SEQ ID NO 95
;; LENGTH: 10
;; TYPE: PRT
;; ORGANISM: Lama glama
US-10-450-036A-95

Query Match
Best Local Similarity 40.8%; Score 29; DB 16; Length 10;
Best Local Similarity 55.6%; Pred. No. 4.7e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 FKLKHYGP 10
Db 2 FKITHYTMG 10

RESULT 11
US-09-910-552-37
;; Sequence 37, Application US/09910552
;; Publication No. US20020197260A1
;; GENERAL INFORMATION:
;; APPLICANT: Granoff, Dan M.
;; APPLICANT: Moe, Gregory R.
;; TITLE OF INVENTION: USE OF MONOCLONAL ANTIBODIES THAT DEFINE UNIQUE
;; TITLE OF INVENTION: MENINGOCOCCAL B EPITOPES IN THE PREPARATION OF VACCINE
;; FILE REFERENCE: 1238.002
;; CURRENT APPLICATION NUMBER: US/09/910,552
;; CURRENT FILING DATE: 2001-07-23
;; PRIOR APPLICATION NUMBER: 09/494,822

;; PRIOR FILING DATE: 2000-01-31
;; NUMBER OF SEQ ID NOS: 68
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 37
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: sequence from
US-09-910-552-37

Query Match
Best Local Similarity 39.4%; Score 28; DB 9; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NFKLKH 6
Db 2 NFKVRL 7

RESULT 12
US-10-643-465-37
;; Sequence 37, Application US/10643465
;; Publication No. US20040077840A1
;; GENERAL INFORMATION:
;; APPLICANT: Granoff, Dan M.
;; APPLICANT: Moe, Gregory R.
;; TITLE OF INVENTION: USE OF MONOCLONAL ANTIBODIES THAT DEFINE UNIQUE
;; TITLE OF INVENTION: MENINGOCOCCAL B EPITOPES IN THE PREPARATION OF VACCINE
;; FILE REFERENCE: 1238.002
;; CURRENT APPLICATION NUMBER: US/10/643,465
;; CURRENT FILING DATE: 2003-08-19
;; PRIOR APPLICATION NUMBER: US/08/925,002
;; PRIOR FILING DATE: 1997-08-27
;; NUMBER OF SEQ ID NOS: 68
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 37
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: sequence from
US-10-643-465-37

Query Match
Best Local Similarity 39.4%; Score 28; DB 16; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NFKLKH 6
Db 2 NFKVRL 7

RESULT 13
US-10-072-419-2
;; Sequence 2, Application US/10072419
;; Publication No. US20030162717A1
;; GENERAL INFORMATION:
;; APPLICANT: Schacter, Bernice
;; APPLICANT: Schacter, Lee
;; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
;; FILE REFERENCE: 10739-1
;; CURRENT APPLICATION NUMBER: US/10/072,419
;; CURRENT FILING DATE: 2002-02-07
;; NUMBER OF SEQ ID NOS: 42
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 2
;; LENGTH: 10
;; TYPE: PRT
;; ORGANISM: Gromphadorhina portentosa

Thu Sep 2 07:41:38 2004

us-09-720-469a-5.aug30.rapb

Page 5

US-10-072-419-2

Query Match 39.4%; Score 28; DB 14; Length 10;
Best Local Similarity 50.0%; Pred. No. 6.9e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 HXPGM 11
DB 3 NFXPGM 8

RESULT 14
US-10-013-312-41
; Sequence 41, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALITA-EID, PIA
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBYTZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193P1B1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 41
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-41

Query Match 38.0%; Score 27; DB 12; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KXHYG 8
DB 1 KLEHFG 6

RESULT 15
US-10-013-312-235
; Sequence 235, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALITA-EID, PIA
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBYTZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193P1B1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 235
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-235

Query Match 38.0%; Score 27; DB 12; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KXHYG 8

DB 1 KLEHFG 6

RESULT 16
US-10-013-312-512
; Sequence 512, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALITA-EID, PIA
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBYTZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193P1B1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 512
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-512

Query Match 38.0%; Score 27; DB 12; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KXHYG 8
DB 3 KLEHFG 6

RESULT 17
US-10-013-312-602
; Sequence 602, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALITA-EID, PIA
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBYTZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193P1B1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 602
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-602

Query Match 38.0%; Score 27; DB 12; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KXHYG 8
DB 3 KLEHFG 6

RESULT 18
US-10-013-312-1404
; Sequence 1404, Application US/10013312

```

; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARI, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1404
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-1404

```

```

Query Match      38.0%; Score 27; DB 12; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 KLEHFG 8
      ||:|:|
Db      1 KLEHFG 6

```

```

RESULT 19
US-10-013-312-1464
; Sequence 1464, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARI, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-1464

```

```

Query Match      38.0%; Score 27; DB 12; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 KLEHFG 8
      ||:|:|
Db      1 KLEHFG 6

```

```

RESULT 20
US-10-013-312-1554
; Sequence 1554, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARI, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
US-10-013-312-1554

```

```

; APPLICANT: JAKOBOWITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1554
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-1554

```

```

Query Match      38.0%; Score 27; DB 12; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 KLEHFG 8
      ||:|:|
Db      1 KLEHFG 6

```

```

RESULT 21
US-10-013-312-1612
; Sequence 1612, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARI, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1612
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-1612

```

```

Query Match      38.0%; Score 27; DB 12; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 KLEHFG 8
      ||:|:|
Db      1 KLEHFG 6

```

```

RESULT 22
US-10-013-312-1672
; Sequence 1672, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARI, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
US-10-013-312-1672

```

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1672
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-013-312-1672

Query Match
Best Local Similarity 38.0%; Score 27; DB 12; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLEHFG 8
||:|:
Db 3 KLEHFG 8

RESULT 23
US-10-013-312-1976
Sequence 1976, Application US/10013312
Publication No. US20030223990A1
GENERAL INFORMATION:
APPLICANT: RAITANO, ARTHUR
APPLICANT: CHALITA-EID, PIA
APPLICANT: PARIS, MARY
APPLICANT: HUBERT, RENE
APPLICANT: GE, WANGMAO
APPLICANT: JAKOBYTZ, AVA
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
TITLE OF INVENTION: 193P1B1B USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20063.00
CURRENT APPLICATION NUMBER: US/10/013,312
CURRENT FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 3005
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1976
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-013-312-1976

Query Match
Best Local Similarity 38.0%; Score 27; DB 12; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLEHFG 8
||:|:
Db 3 KLEHFG 8

RESULT 24
US-10-013-312-52
Sequence 52, Application US/10013312
Publication No. US20030223990A1
GENERAL INFORMATION:
APPLICANT: RAITANO, ARTHUR
APPLICANT: CHALITA-EID, PIA
APPLICANT: PARIS, MARY
APPLICANT: HUBERT, RENE
APPLICANT: GE, WANGMAO
APPLICANT: JAKOBYTZ, AVA
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
TITLE OF INVENTION: 193P1B1B USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20063.00
CURRENT APPLICATION NUMBER: US/10/013,312
CURRENT FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 3005
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 52
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-10-013-312-52

Query Match
Best Local Similarity 38.0%; Score 27; DB 12; Length 10;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLEHFG 8
||:|:
Db 1 KLEHFG 6

RESULT 25
US-10-013-312-183
Sequence 183, Application US/10013312
Publication No. US20030223990A1
GENERAL INFORMATION:
APPLICANT: RAITANO, ARTHUR
APPLICANT: CHALITA-EID, PIA
APPLICANT: PARIS, MARY
APPLICANT: HUBERT, RENE
APPLICANT: GE, WANGMAO
APPLICANT: JAKOBYTZ, AVA
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
TITLE OF INVENTION: 193P1B1B USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20063.00
CURRENT APPLICATION NUMBER: US/10/013,312
CURRENT FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 3005
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 183
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-10-013-312-183

Query Match
Best Local Similarity 38.0%; Score 27; DB 12; Length 10;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLEHFG 8
||:|:
Db 4 KLEHFG 9

RESULT 26
US-10-013-312-254
Sequence 254, Application US/10013312
Publication No. US20030223990A1
GENERAL INFORMATION:
APPLICANT: RAITANO, ARTHUR
APPLICANT: CHALITA-EID, PIA
APPLICANT: PARIS, MARY
APPLICANT: HUBERT, RENE
APPLICANT: GE, WANGMAO
APPLICANT: JAKOBYTZ, AVA
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
TITLE OF INVENTION: 193P1B1B USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20063.00
CURRENT APPLICATION NUMBER: US/10/013,312
CURRENT FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 3005
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 254
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-10-013-312-254

Query Match
Best Local Similarity 38.0%; Score 27; DB 12; Length 10;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLEHFG 8
||:|:
Db 1 KLEHFG 6

RESULT 27
US-10-013-312-384
; Sequence 384, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALILITA-EID, PIA
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 384
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-384

Query Match 38.0%; Score 27; DB 12; Length 10;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLRHVG 8
||:|:
Db 4 KLRHVG 9

RESULT 28
US-10-013-312-497
; Sequence 497, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALILITA-EID, PIA
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 497
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-497

Query Match 38.0%; Score 27; DB 12; Length 10;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLRHVG 8
||:|:
Db 4 KLRHVG 9

RESULT 29
US-10-013-312-664
; Sequence 664, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALILITA-EID, PIA
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED

; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALILITA-EID, PIA
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 664
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-664

Query Match 38.0%; Score 27; DB 12; Length 10;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLRHVG 8
||:|:
Db 3 KLRHVG 6

RESULT 30
US-10-013-312-686
; Sequence 686, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALILITA-EID, PIA
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 686
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-686

Query Match 38.0%; Score 27; DB 12; Length 10;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLRHVG 8
||:|:
Db 1 KLRHVG 6

RESULT 31
US-10-013-312-2094
; Sequence 2094, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALILITA-EID, PIA
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOWITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED

```
/ TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER
/ FILE REFERENCE: 51158-20063.00
/ CURRENT APPLICATION NUMBER: US/10/013,312
/ CURRENT FILING DATE: 2002-05-30
/ NUMBER OF SEQ ID NOS: 3005
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2094
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-013-312-2094

Query Match
Best Local Similarity 38.0%; Score 27; DB 12; Length 10;
Best Local Similarity 66.7%; Pred. No. 1e+03; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 0;

Qy 3 KXKHYG 8
Db 1 KLEHFG 6

RESULT 32
US-10-013-312-2114
/ Sequence 2114, Application US/10013312
/ Publication No. US2003022390A1
/ GENERAL INFORMATION:
/ APPLICANT: RAITANO, ARTHUR
/ APPLICANT: CHALLITA-ETD, PIA
/ APPLICANT: PARIS, MARY
/ APPLICANT: HUBERT, RENE
/ APPLICANT: GE, WANGMAO
/ APPLICANT: JAKOBOVITZ, AVA
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
/ TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER
/ FILE REFERENCE: 51158-20063.00
/ CURRENT APPLICATION NUMBER: US/10/013,312
/ CURRENT FILING DATE: 2002-05-30
/ NUMBER OF SEQ ID NOS: 3005
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2114
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-013-312-2114

Query Match
Best Local Similarity 38.0%; Score 27; DB 12; Length 10;
Best Local Similarity 66.7%; Pred. No. 1e+03; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 0;

Qy 3 KXKHYG 8
Db 4 KLEHFG 9

RESULT 33
US-10-013-312-2217
/ Sequence 2217, Application US/10013312
/ Publication No. US2003022390A1
/ GENERAL INFORMATION:
/ APPLICANT: RAITANO, ARTHUR
/ APPLICANT: CHALLITA-ETD, PIA
/ APPLICANT: PARIS, MARY
/ APPLICANT: HUBERT, RENE
/ APPLICANT: GE, WANGMAO
/ APPLICANT: JAKOBOVITZ, AVA
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
/ TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER
/ FILE REFERENCE: 51158-20063.00
/ CURRENT APPLICATION NUMBER: US/10/013,312
/ CURRENT FILING DATE: 2002-05-30
/ NUMBER OF SEQ ID NOS: 3005
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2217
```

```
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-013-312-2217

Query Match
Best Local Similarity 38.0%; Score 27; DB 12; Length 10;
Best Local Similarity 66.7%; Pred. No. 1e+03; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 0;

Qy 3 KXKHYG 8
Db 1 KLEHFG 6

RESULT 34
US-10-013-312-2250
/ Sequence 2250, Application US/10013312
/ Publication No. US2003022390A1
/ GENERAL INFORMATION:
/ APPLICANT: RAITANO, ARTHUR
/ APPLICANT: CHALLITA-ETD, PIA
/ APPLICANT: PARIS, MARY
/ APPLICANT: HUBERT, RENE
/ APPLICANT: GE, WANGMAO
/ APPLICANT: JAKOBOVITZ, AVA
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
/ TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER
/ FILE REFERENCE: 51158-20063.00
/ CURRENT APPLICATION NUMBER: US/10/013,312
/ CURRENT FILING DATE: 2002-05-30
/ NUMBER OF SEQ ID NOS: 3005
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2250
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-013-312-2250

Query Match
Best Local Similarity 38.0%; Score 27; DB 12; Length 10;
Best Local Similarity 66.7%; Pred. No. 1e+03; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 0;

Qy 3 KXKHYG 8
Db 1 KLEHFG 6

RESULT 35
US-10-013-312-2321
/ Sequence 2321, Application US/10013312
/ Publication No. US2003022390A1
/ GENERAL INFORMATION:
/ APPLICANT: RAITANO, ARTHUR
/ APPLICANT: CHALLITA-ETD, PIA
/ APPLICANT: PARIS, MARY
/ APPLICANT: HUBERT, RENE
/ APPLICANT: GE, WANGMAO
/ APPLICANT: JAKOBOVITZ, AVA
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
/ TITLE OF INVENTION: 193P1E1B USEFUL IN TREATMENT AND DETECTION OF CANCER
/ FILE REFERENCE: 51158-20063.00
/ CURRENT APPLICATION NUMBER: US/10/013,312
/ CURRENT FILING DATE: 2002-05-30
/ NUMBER OF SEQ ID NOS: 3005
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2321
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-013-312-2321

Query Match
Best Local Similarity 38.0%; Score 27; DB 12; Length 10;
Best Local Similarity 66.7%; Pred. No. 1e+03; Indels 0; Gaps 0;
```

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KXKHYG 8
||:|:|
Db 4 KLEHFG 9

RESULT 36
US-10-013-312-2339
; Sequence 2339, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE REFERENCE: 51158-20063.00
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2339
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-2339

Query Match 38.0%; Score 27; DB 12; Length 10;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KXKHYG 8
||:|:|
Db 1 KLEHFG 6

RESULT 37
US-10-013-312-2407
; Sequence 2407, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE REFERENCE: 51158-20063.00
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2407
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-2407

Query Match 38.0%; Score 27; DB 12; Length 10;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KXKHYG 8
||:|:|
Db 5 KLEHFG 10

RESULT 38
US-10-360-101-155
; Sequence 155, Application US/10360101
; Publication No. US20040009550A1
; GENERAL INFORMATION:
; APPLICANT: MOLL, GERT N.
; APPLICANT: LEENHOUTS, CORNELIS J.
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
; FILE REFERENCE: 2183-5673
; CURRENT APPLICATION NUMBER: US/10/360,101
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02077060.8
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 155
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: (Q1,A4,S5,C8)-sequence of LHRH2
US-10-360-101-155

Query Match 38.0%; Score 27; DB 15; Length 10;
Best Local Similarity 42.9%; Pred. No. 1e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 KHYGPGM 11
:|:|:|
Db 1 QHMASGM 7

RESULT 39
US-10-360-101-156
; Sequence 156, Application US/10360101
; Publication No. US20040009550A1
; GENERAL INFORMATION:
; APPLICANT: MOLL, GERT N.
; APPLICANT: LEENHOUTS, CORNELIS J.
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
; FILE REFERENCE: 2183-5673
; CURRENT APPLICATION NUMBER: US/10/360,101
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02077060.8
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 156
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: (Q1,A4,S5,C9)-sequence of LHRH2
US-10-360-101-156

Query Match 38.0%; Score 27; DB 15; Length 10;
Best Local Similarity 42.9%; Pred. No. 1e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 KHYGPGM 11
:|:|:|
Db 1 QHMASGM 7

RESULT 40
US-10-360-101-157
; Sequence 157, Application US/10360101
; Publication No. US20040009550A1
; GENERAL INFORMATION:
; APPLICANT: MOLL, GERT N.
; APPLICANT: LEENHOUTS, CORNELIS J.
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
; FILE REFERENCE: 2183-5673
US-10-360-101-157

;; CURRENT APPLICATION NUMBER: US/10/360,101
;; PRIOR FILING DATE: 2003-02-07
;; PRIOR APPLICATION NUMBER: EP 02077060.8
;; PRIOR FILING DATE: 2002-05-24
;; NUMBER OF SEQ ID NOS: 309
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 157
;; LENGTH: 10
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: (Q1,A4,S5,C10)-sequence of LHRH2
US-10-360-101-157

Query Match 38.0%; Score 27; DB 15; Length 10;
Best Local Similarity 42.9%; Pred. No. 1e+03; 2; Indels 0; Gaps 0;
Matches 3; Conservative 2; Mismatches 2;

QY 5 KHYGPGW 11
:|:|
Db 1 QHWASGW 7

RESULT 41
US-10-723-434-113
; Sequence 113, Application US/10723434
; Publication No. US2004013357A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Pingyu
; APPLICANT: Luo, Peizhi
; APPLICANT: Wang, Kevin C.
; APPLICANT: Hsieh, Mark
; APPLICANT: Li, Yan
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
; FILE REFERENCE: 26050-709.501
; CURRENT APPLICATION NUMBER: US/10/723,434
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 10/153,176
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/443,134
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 113
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH/CDR1
US-10-723-434-113

Query Match 39.0%; Score 27; DB 16; Length 10;
Best Local Similarity 57.1%; Pred. No. 1e+03; 2; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 2;

QY 2 FKLKHYG 8
:|:|
Db 2 YSLDHYG 8

RESULT 42
US-10-723-434-132
; Sequence 132, Application US/10723434
; Publication No. US2004013357A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Pingyu
; APPLICANT: Luo, Peizhi
; APPLICANT: Wang, Kevin C.
; APPLICANT: Hsieh, Mark

;; APPLICANT: Li, Yan
;; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
;; FILE REFERENCE: 26050-709.501
;; CURRENT APPLICATION NUMBER: US/10/723,434
;; CURRENT FILING DATE: 2003-11-26
;; PRIOR APPLICATION NUMBER: US 60/284,407
;; PRIOR FILING DATE: 2001-04-17
;; PRIOR APPLICATION NUMBER: US 10/125,687
;; PRIOR FILING DATE: 2002-04-17
;; PRIOR APPLICATION NUMBER: US 10/153,176
;; PRIOR FILING DATE: 2002-05-20
;; PRIOR APPLICATION NUMBER: US 10/443,134
;; PRIOR FILING DATE: 2003-05-20
;; NUMBER OF SEQ ID NOS: 156
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 132
;; LENGTH: 10
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: VH/CDR1
US-10-723-434-132

Query Match 38.0%; Score 27; DB 16; Length 10;
Best Local Similarity 57.1%; Pred. No. 1e+03; 2; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 2;

QY 2 FKLKHYG 8
:|:|
Db 2 YDLSHYG 8

RESULT 43
US-10-286-457-132
; Sequence 132, Application US/10286457
; Publication No. US20030166004A1
; GENERAL INFORMATION:
; APPLICANT: JENO GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
; FILE REFERENCE: GPCI-P01-178
; CURRENT APPLICATION NUMBER: US/10/286,457
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 684
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 132
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ability to selectively bind to endothelial cells
US-10-286-457-132

Query Match 38.0%; Score 27; DB 14; Length 12;
Best Local Similarity 44.4%; Pred. No. 1.2e+03; 2; Indels 0; Gaps 0;
Matches 4; Conservative 3; Mismatches 2;

QY 1 NFKLKHYGP 9
:|:|
Db 4 NYKIRSGGP 12

RESULT 44
US-10-182-252A-200
; Sequence 200, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE

```

; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182, 252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 200
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-200

```

```

Query Match          36.6%; Score 26; DB 12; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      6 HYPG 10
|      |
|      |
Db      1 HIGPG 5

```

```

RESULT 45
US-10-062-710-162
; Sequence 162, Application US/10062710
; Publication No. US20030049253A1
; GENERAL INFORMATION:
; APPLICANT: Li, Frank O.
; APPLICANT: Chu, Yong-Liang
; APPLICANT: Qiu, Jian-Tai
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of
; TITLE OF INVENTION: MHC-Recognized Epitopes
; TITLE OF INVENTION: Via Peptide Vaccines
; FILE REFERENCE: 3781-001-27
; CURRENT APPLICATION NUMBER: US/10/062,710
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/310,498
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 162
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV B Cell Epitopes
US-10-062-710-162

```

```

Query Match          36.6%; Score 26; DB 14; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

Qy      6 HYPG 10
|      |
|      |
Db      3 HIGPG 7

```

Search completed: August 30, 2004, 11:04:57
Job time : 14.4527 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:59 ; Search time 4.34797 Seconds
(without alignments)
130.609 Million cell updates/sec

Title: US-09-720-469a-5

Perfect score: 71

Sequence: 1 NFKLHXGPGW 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 segs, 51625971 residues

Total number of hits satisfying chosen parameters: 78885

Minimum DB seq length: 8

Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents, AA:*
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	52.1	14	5	PCT-US93-06751-120
2	35	49.3	9	1	US-07-863-324-2
3	32	45.1	14	5	PCT-US93-06751-67
4	31	43.7	8	1	US-08-975-9628-2
5	31	43.7	8	1	US-08-562-1148-2
6	31	43.7	8	3	US-08-729-594A-2
7	31	43.7	8	1	US-08-937-993-2
8	30	42.3	8	1	US-08-271-830-56
9	30	42.3	13	5	PCT-US93-06751-65
10	29	40.8	14	5	PCT-US93-06751-93
11	29	40.8	10	1	US-08-353-400-26
12	29	40.8	14	5	PCT-US93-06751-65
13	29	40.8	14	5	PCT-US93-06751-103
14	28	39.4	8	4	US-08-925-002-37
15	28	39.4	8	4	US-08-910-552-37
16	28	39.4	10	2	US-08-747-137-122
17	28	39.4	11	2	US-08-598-873-68
18	28	39.4	11	3	US-08-605-430-68
19	28	39.4	14	5	PCT-US93-06751-63
20	28	39.4	14	5	PCT-US93-06751-104
21	27	38.0	9	3	US-08-159-339A-391
22	27	38.0	13	5	PCT-US93-06751-102
23	26	36.6	8	1	US-08-279-906A-5
24	26	36.6	8	5	PCT-US92-06688-8
25	26	36.6	9	1	US-08-318-970B-23
26	26	36.6	9	3	US-08-946-525-4
27	26	36.6	9	3	US-09-082-279B-920

28	26	36.6	9	4	US-09-315-304B-920	Sequence 920, App
29	26	36.6	9	4	US-09-599-286-4	Sequence 4, Appl
30	26	36.6	9	4	US-09-834-784-920	Sequence 920, App
31	26	36.6	9	4	US-09-515-965A-920	Sequence 920, App
32	26	36.6	9	4	US-09-350-641C-920	Sequence 94, Appl
33	26	36.6	10	1	US-08-250-789A-94	Sequence 15, Appl
34	26	36.6	10	1	US-08-341-219-15	Sequence 15, Appl
35	26	36.6	10	1	US-08-341-219-16	Sequence 23, Appl
36	26	36.6	10	1	US-08-253-030-23	Sequence 23, Appl
37	26	36.6	10	1	US-08-253-030-25	Sequence 19, Appl
38	26	36.6	10	2	US-08-425-069-19	Sequence 19, Appl
39	26	36.6	10	2	US-08-687-559-10	Sequence 19, Appl
40	26	36.6	10	2	US-08-317-844B-19	Sequence 15, Appl
41	26	36.6	10	3	US-08-946-525-15	Sequence 15, Appl
42	26	36.6	10	3	US-08-912-314A-15	Sequence 15, Appl
43	26	36.6	10	3	US-08-912-314A-16	Sequence 16, Appl
44	26	36.6	10	4	US-09-599-286-15	Sequence 15, Appl
45	26	36.6	10	4	US-09-401-415-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
PCT-US93-06751-120
Sequence 120, Application PC/TUS9306751
GENERAL INFORMATION:
APPLICANT: P. Keller, A. J. Conley, A. R. Shaw, B. A. Arnold
TITLE OF INVENTION: Immunological Conjugates of OMpe and
TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GxG Epitopes
NUMBER OF SEQUENCES: 146
CORRESPONDENCE ADDRESS:
ADDRESS: Merck & Co., Inc.
STREET: P. O. Box 2000
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06751
FILING DATE: 19930719
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Meredich, Roy D.
REGISTRATION NUMBER: 30,777
REFERENCE/DOCKET NUMBER: 18614
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4678
TELEFAX: (908) 594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO: 120:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE: Random Epitope Library Beta
PCT-US93-06751-120

Query Match 52.1%; Score 37; DB 5; Length 14;
Best Local Similarity 55.6%; Pred. No. 6.2;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
2 FKLHXGPG 10
:: |||||

Db 3 YRAHYGPG 11

RESULT 2

US-07-963-324-2
Sequence 2, Application US/07963324
Patent No. 5274122

GENERAL INFORMATION:

APPLICANT: Marburg, Stephen
APPLICANT: Leanza, William J
APPLICANT: Tolman, Richard L
TITLE OF INVENTION: Acidic Derivatives of Homocysteine
TITLE OF INVENTION: Thiolactone
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Merck & Co., Inc.
STREET: 126 Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/963,324

FILING DATE: 19921015

ATTORNEY/AGENT INFORMATION:

NAME: Benzen, Gerard H
REGISTRATION NUMBER: 35,746

REFERENCE/DOCKET NUMBER: 18787

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 594-3901

TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: AMINO ACID

TOPOLOGY: both

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1

OTHER INFORMATION: /label= Nle

OTHER INFORMATION: /note= "norleucine"

FEATURE:

NAME/KEY: Cyste-links

LOCATION: 2..9

OTHER INFORMATION: /label= cycle

OTHER INFORMATION: /note= "amide bond through lys epsilon amino"

US-07-963-324-2

Query Match 49.3%; Score 35; DB 1; Length 9;
Best Local Similarity 85.7%; Pred. No. 3a+05; 1; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;QY 4 LKHYGPG 10
1 LKHIGPG 7

RESULT 3

PCT-US93-06751-67

Sequence 67, Application PC/TUS9306751

GENERAL INFORMATION:

APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold

TITLE OF INVENTION: Immunological Conjugates of OMPC and

TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GXG Epitopes

NUMBER OF SEQUENCES: 146

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Merck & Co., Inc.

STREET: P.O. Box 2000

CITY: Rahway

STATE: NJ

COUNTRY: USA

ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/06751

FILING DATE: 19930719

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Weredith, Roy D.

REGISTRATION NUMBER: 30,777

REFERENCE/DOCKET NUMBER: 18614

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 594-4678

TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 67:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

IMMEDIATE SOURCE: Random Epitope Library Gamma

PCT-US93-06751-67

Query Match 45.1%; Score 32; DB 5; Length 14;
Best Local Similarity 71.4%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;QY 3 KLNHYGP 9
1 KANHYGP 7

RESULT 4

US-08-375-962B-2

Sequence 2, Application US/08375962B

Patent No. 5731195

GENERAL INFORMATION:

APPLICANT: CHRISTER, ERIKSSON, ULF

TITLE OF INVENTION: Isolated Nucleic Acid Molecule

TITLE OF INVENTION: Which Codes for A 32 kDa Protein Having 11-CIS Retinol

TITLE OF INVENTION: Dehydrogenase Activity, and Which Associates With P63,

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Felfe & Lynch

STREET: 805 Third Avenue

CITY: New York City

STATE: New York

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage

COMPUTER: IBM

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect (ASCII standard)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/375,962B

FILING DATE: 20-January-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/258,418
FILING DATE: 6-October-1994
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5372.1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-375-962B-2

Query Match 43.7%; Score 31; DB 1; Length 8;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 YPGW 11
|
|
|
|
DB 1 YSPGW 5

RESULT 5
US-08-562-114B-2

; Sequence 2, Application US/08562114B

; Patent No. 5972646

; GENERAL INFORMATION:

; APPLICANT: ERIKSSON ET AL.

; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE WHICH CODES FOR A

; TITLE OF INVENTION: 32 KDA PROTEIN HAVING 11-CIS RETINOL HYDROGENASE

; TITLE OF INVENTION: ACTIVITY, AND WHICH ASSOCIATES WITH P63, A

; TITLE OF INVENTION: PORTION OF A RETINOL BINDING PROTEIN RECEPTOR

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felle & Lynch

; STREET: 805 Third Avenue

; CITY: New York City

; STATE: New York

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage

; COMPUTER: IBM

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: Wordperfect 5.1 and ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/562,114B

; FILING DATE: 22-No. 5972646ember-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/375,962

; FILING DATE: 20-January-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Kohl, Vineet

; REGISTRATION NUMBER: 37,003

; REFERENCE/DOCKET NUMBER: LUD 5372.2 CIP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 688-9200

; TELEFAX: (212) 838-3884

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-562-114B-2

Query Match 43.7%; Score 31; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 YPGW 11
|
|
|
|
DB 1 YSPGW 5

RESULT 6
US-08-729-594A-2

; Sequence 2, Application US/08729594A

; Patent No. 6280997

; GENERAL INFORMATION:

; APPLICANT: Eriksson, Ulf, Simon, Andreas, Romert, Anna

; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE WHICH

; TITLE OF INVENTION: CODES FOR A 32 KDA PROTEIN HAVING 11-CIS RETINOL DEHYDROGENASE

; TITLE OF INVENTION: ACTIVITY, AND WHICH ASSOCIATES WITH P63, A PORTION OF A

; TITLE OF INVENTION: RETINOL BINDING PROTEIN RECEPTOR

; NUMBER OF SEQUENCES: 41

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felle & Lynch

; STREET: 805 Third Avenue

; CITY: New York City

; STATE: New York

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage

; COMPUTER: IBM

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/729,594A

; FILING DATE: 11-October-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/562,114

; FILING DATE: 22-No. 6280997ember-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/375,962

; FILING DATE: 20-January-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/258,418

; FILING DATE: 10-June-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Hanson, No. 6280997man D.

; REGISTRATION NUMBER: 30,946

; REFERENCE/DOCKET NUMBER: LUD 5372.3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 688-9200

; TELEFAX: (212) 838-3884

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-729-594A-2

Query Match 43.7%; Score 31; DB 3; Length 8;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 YPGW 11
|
|
|
|
DB 1 YSPGW 5

RESULT 7
US-08-937-993-2

; Sequence 2, Application US/08937993

; Patent No. 6399344

; GENERAL INFORMATION:

APPLICANT: Eriksson, Ulf; Simon, Andras; Romert, Anna
TITLE OF INVENTION: ISOLATED PROTEINS HAVING CIS-R
TITLE OF INVENTION: DEHYDROGENASE ACTIVITY
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,993
FILING DATE: September 26, 1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/729,594
FILING DATE: 11-October-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/562,114
FILING DATE: 22-No. 6399344ember-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/375,962
FILING DATE: 20-January-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/258,418
FILING DATE: 10-June-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6399344man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 668-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-937-993-2

Query Match 43.7%; Score 31; DB 4; Length 8;
Best Local Similarity 80.0%; Pred.No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0,
QY 7 YSPGW 11
Db 1 YSPGW 5

RESULT 8
US-08-271-830-56
Sequence 56; Application US/08271830
Patent No. 5510332
GENERAL INFORMATION:
APPLICANT: Kogan, Timothy P.
APPLICANT: Ren, Kaijun
APPLICANT: Vanderslice, Peter
APPLICANT: Beck, Pamela J.
TITLE OF INVENTION: A PROCESS OF INHIBITING THE BINDING OF THE
TITLE OF INVENTION: INTEGRIN '4 1 TO VCAM OR FIBRONECTIN AND
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Shore & Milnarcow, Ltd.
STREET: 180 No. 5510332th Steeton, Suite 4700
CITY: Chicago
STATE: IL

```

1  COUNTRY: USA
2  ZIP: 60601
3  COMPUTER READABLE FORM:
4  MEDIUM TYPE: Floppy disk
5  COMPUTER: IBM PC compatible
6  OPERATING SYSTEM: PC-DOS/MS-DOS
7  SOFTWARE: Patentin Release #1.0, Version #1.25
8  CURRENT APPLICATION DATA:
9  APPLICATION NUMBER: US/08/271,830
10 FILING DATE:
11 CLASSIFICATION: 435
12 ATTORNEY/AGENT INFORMATION:
13 NAME: No. 5510332chup, Thomas E.
14 REGISTRATION NUMBER: 33,268
15 TELECOMMUNICATION INFORMATION:
16 TELEPHONE: (312)616-5400
17 TELEFAX: (312)616-5460
18 INFORMATION FOR SEQ ID NO: 56:
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 8 amino acids
21 TYPE: amino acid
22 TOPOLOGY: linear
23 MOLECULE TYPE: peptide
24 FEATURE:
25 NAME/KEY: Modified-site
26 LOCATION: 8
27 OTHER INFORMATION: //label=Xaa
28 OTHER INFORMATION: /note="Xaa=Pro-NH2."
29 US-08-271-830-56
30
31 Query Match 42.3% Score 30, DB 1; Length 8;
32 Best Local Similarity 100.0%; Pred.No.3e+05;
33 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
34
35 Cy 8 GPCW 11
36 ||||
37 Db 1 GPCW 4
38
39 RESULT 9
40 PCT-US93-06751-66
41 Sequence 66, Application PC/TUS9306751
42 GENERAL INFORMATION:
43 APPLICANT: P. Keller, A. J. Conley, A. R. Shaw, B. A. Arnold
44 TITLE OF INVENTION: Immunological Conjugates of OmpC and
45 TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GxG Epitopes
46 NUMBER OF SEQUENCES: 146
47 CORRESPONDENCE ADDRESS:
48 ADDRESSEE: Merck & Co., Inc.
49 STREET: P.O. Box 2000
50 CITY: Rahway
51 STATE: NJ
52 COUNTRY: USA
53 ZIP: 07065
54 COMPUTER READABLE FORM:
55 MEDIUM TYPE: Floppy disk
56 COMPUTER: IBM PC compatible
57 OPERATING SYSTEM: PC-DOS/MS-DOS
58 SOFTWARE: Patentin Release #1.0, Version #1.25
59 CURRENT APPLICATION DATA:
60 APPLICATION NUMBER: PCT/US93/06751
61 FILING DATE: 19930719
62 CLASSIFICATION:
63 ATTORNEY/AGENT INFORMATION:
64 NAME: Meredith, Roy D.
65 REGISTRATION NUMBER: 30,777
66 REFERENCE/DOCKET NUMBER: 18614
67 TELECOMMUNICATION INFORMATION:
68 TELEPHONE: (908) 594-4678
69 TELEFAX: (908) 594-4720
70 TELEX: 138825
71 INFORMATION FOR SEQ ID NO: 66:
72 SEQUENCE CHARACTERISTICS:

```

LENGTH: 13 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 IMMEDIATE SOURCE: Random Epitope Library Delta
 PCT-US93-06751-66

Query Match 42.3%; Score 30; DB 5; Length 13;
 Best Local Similarity 80.0%; Pred. No. 86;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 HYGPG 10
 Db 4 HFGPG 8

RESULT 10
 PCT-US93-06751-93
 Sequence 93, Application PC/TUS9306751
 GENERAL INFORMATION:
 APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold
 TITLE OF INVENTION: Immunological Conjugates of OmpC and
 TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GXG Epitopes
 NUMBER OF SEQUENCES: 146
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Merck & Co., Inc.
 STREET: P.O. Box 2000
 CITY: Rahway
 STATE: NJ
 COUNTRY: USA
 ZIP: 07065
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/06751
 FILING DATE: 19930719
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Weidlich, Roy D.
 REGISTRATION NUMBER: 30,777
 REFERENCE/DOCKET NUMBER: 18614
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-4678
 TELEFAX: (908) 594-4720
 TELEX: 138825
 INFORMATION FOR SEQ ID NO: 93:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 IMMEDIATE SOURCE: Random Epitope Library Gamma
 PCT-US93-06751-93

Query Match 42.3%; Score 30; DB 5; Length 14;
 Best Local Similarity 80.0%; Pred. No. 92;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 HYGPG 10
 Db 4 HFGPG 8

RESULT 11

US-08-353-400-26
 Sequence 26, Application US/08353400
 Patent No. 5665357
 GENERAL INFORMATION:
 APPLICANT:
 TITLE OF INVENTION: PROTEINS
 NUMBER OF SEQUENCES: 37
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/353,400
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9324819.3
 FILING DATE: 03-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9411089.7
 FILING DATE: 03-JUN-1994
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-353-400-26

Query Match 40.8%; Score 29; DB 1; Length 10;
 Best Local Similarity 57.1%; Pred. No. 98;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 KHYGPGW 11
 Db 3 EHRGSGW 9

RESULT 12
 PCT-US93-06751-65
 Sequence 65, Application PC/TUS9306751
 GENERAL INFORMATION:
 APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold
 TITLE OF INVENTION: Immunological Conjugates of OmpC and
 TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GXG Epitopes
 NUMBER OF SEQUENCES: 146
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Merck & Co., Inc.
 STREET: P.O. Box 2000
 CITY: Rahway
 STATE: NJ
 COUNTRY: USA
 ZIP: 07065
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/06751
 FILING DATE: 19930719
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Weidlich, Roy D.
 REGISTRATION NUMBER: 30,777
 REFERENCE/DOCKET NUMBER: 18614
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-4678
 TELEFAX: (908) 594-4720
 TELEX: 138825
 INFORMATION FOR SEQ ID NO: 65:

SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE: Random Epitope Library Delta
PCT-US93-06751-65

Query Match 40.8%; Score 29; DB 5; Length 14;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 HYKPG 10
Db 4 HWKPG 8

RESULT 13
PCT-US93-06751-103
Sequence 103, Application PC/TUS9306751
GENERAL INFORMATION:
APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold
TITLE OF INVENTION: Immunological Conjugates of OMPc and
TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GXG Epitopes
NUMBER OF SEQUENCES: 146
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06751
FILING DATE: 19930719

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Meredith, Roy D.
REGISTRATION NUMBER: 30,777
REFERENCE/DOCKET NUMBER: 18614
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4678
TELEFAX: (908) 594-4720
TELEX: 138825

INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE: Random Epitope Library Delta
PCT-US93-06751-103

Query Match 40.8%; Score 29; DB 5; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 KUKHYGPG 10
Db 1 EVHYGPG 8

RESULT 14
US-08-925-002-37
Sequence 37, Application US/08925002
Patent No. 6048527
GENERAL INFORMATION:
APPLICANT: Granoff, Dan M.
TITLE OF INVENTION: USE OF MONOCLONAL ANTIBODIES THAT DEFINE UNIQUE
TITLE OF INVENTION: MENINGOCOCCAL B EPIPTOPES IN THE PREPARATION OF VACCINE
TITLE OF INVENTION: COMPOSITIONS
FILE REFERENCE: 1238,002
CURRENT APPLICATION NUMBER: US/08/925,002
CURRENT FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 68
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 37
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: sequence from
US-08-925-002-37

Query Match 39.4%; Score 28; DB 3; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NFKLKH 6
Db 2 NFKVRH 7

RESULT 15
US-09-910-552-37
Sequence 37, Application US/09910552
Patent No. 6642354
GENERAL INFORMATION:
APPLICANT: Granoff, Dan M.
TITLE OF INVENTION: USE OF MONOCLONAL ANTIBODIES THAT DEFINE UNIQUE
TITLE OF INVENTION: MENINGOCOCCAL B EPIPTOPES IN THE PREPARATION OF VACCINE
TITLE OF INVENTION: COMPOSITIONS
FILE REFERENCE: 1238,002
CURRENT APPLICATION NUMBER: US/09/910,552
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: 09/494,822
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 68
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 37
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: sequence from
US-09-910-552-37

Query Match 39.4%; Score 28; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NFKLKH 6
Db 2 NFKVRH 7

RESULT 16
US-08-747-137-122
Sequence 122, Application US/08747137
Patent No. 5945033
GENERAL INFORMATION:

APPLICANT: YEN, Richard C.K.
TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
THERAPEUTIC AND DIAGNOSTIC USE
NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,137
FILING DATE: 12-NOV-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,546
FILING DATE: 14-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/069,831
FILING DATE: 01-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/959,560
FILING DATE: 13-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/641,720
FILING DATE: 15-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 016197-000840US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /product= "p-Glu"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: /product= "thr-Amide"
US-08-747-137-122

Query Match 39.4%; Score 28; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 HYPGW 11
DB 3 NPSGW 8

RESULT 17
US-08-598-873-68
Sequence 68, Application US/08598873
Patent No. 5928884
GENERAL INFORMATION:
APPLICANT: Croce, Carlo M.
ATTORNEY/AGENT INFORMATION:
NAME: Huebner, Kay
REGISTRATION NUMBER: 29,258
REFERENCE/DOCKET NUMBER: 8666-005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/598,873
FILING DATE: 09-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Friebel, Thomas E.
REGISTRATION NUMBER: 29,258
REFERENCE/DOCKET NUMBER: 8666-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-598-873-68

Query Match 39.4%; Score 28; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HYPG 9
DB 1 HYPG 4

RESULT 18
US-08-605-430-68
Sequence 68, Application US/08605430
Patent No. 6242212
GENERAL INFORMATION:
APPLICANT: Croce, Carlo M.
ATTORNEY/AGENT INFORMATION:
NAME: Huebner, Kay
REGISTRATION NUMBER: 29,258
REFERENCE/DOCKET NUMBER: 8666-005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNITE
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-605-430-68

Query Match 39.4%; Score 28; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HXGP 9
: ||||
DB 1 HXGP 4

RESULT 19
PCT-US93-06751-63
Sequence 63, Application PC/TUS9306751
GENERAL INFORMATION:
APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold
TITLE OF INVENTION: Immunological Conjugates of OmpC and
TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GxG Epitopes
NUMBER OF SEQUENCES: 146
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06751
FILING DATE: 19930719
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Meredith, Roy D.
REGISTRATION NUMBER: 30,777
REFERENCE/DOCKET NUMBER: 18614
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4678
TELEFAX: (908) 594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE: Random Epitope Library Delta
PCT-US93-06751-63

Query Match 39.4%; Score 28; DB 5; Length 14;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGP 10
: ||||
DB 3 RHGPG 8

RESULT 20

PCT-US93-06751-104
Sequence 104, Application PC/TUS9306751
GENERAL INFORMATION:
APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold
TITLE OF INVENTION: Immunological Conjugates of OmpC and
TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GxG Epitopes
NUMBER OF SEQUENCES: 146
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06751
FILING DATE: 19930719
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Meredith, Roy D.
REGISTRATION NUMBER: 30,777
REFERENCE/DOCKET NUMBER: 18614
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4678
TELEFAX: (908) 594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE: Random Epitope Library Delta
PCT-US93-06751-104

Query Match 39.4%; Score 28; DB 5; Length 14;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGP 10
: ||||
DB 3 RHGPG 8

RESULT 21
US-08-159-339A-391
Sequence 391, Application US/08159339A
Patent No. 6037135
GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard W.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esben
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:
INFORMATION FOR SEQ ID NO: 391:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-391

Query Match      38.0%; Score 27; DB 3; Length 9;
Best Local Similarity 66.7%; Pred. No. 3e+05; 1; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 1; Indels 0;

QY      2 PFKLHY 7
      |||
      3 FKKRHY 8
      |||

Db      3 FKKRHY 8

RESULT 22
PCT-US93-06751-102
Sequence 102, Application PC/TUS9306751
GENERAL INFORMATION:
APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold
TITLE OF INVENTION: Immunological Conjugates of CMPC and
TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GXG Epitopes
NUMBER OF SEQUENCES: 146
CORRESPONDENCE ADDRESS:
ADDRESSER: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06751
FILING DATE: 19930719
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Meredith, Roy D.
REGISTRATION NUMBER: 30,777
REFERENCE/DOCKET NUMBER: 18614
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4678
TELEFAX: (908) 594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO: 102:
```

```
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE: Random Epitope Library Delta
PCT-US93-06751-102

Query Match      38.0%; Score 27; DB 5; Length 13;
Best Local Similarity 80.0%; Pred. No. 2.7e+02; 0; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0; Indels 0;

QY      6 HYRPG 10
      |||
      4 NYRPG 8

Db      4 NYRPG 8

RESULT 23
US-08-279-906A-5
Sequence 5, Application US/08279906A
Patent No. 5618922
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
APPLICANT: Terada, Masaki
APPLICANT: Yoneda, Yukio
TITLE OF INVENTION: NM03 Antibody Materials and Methods
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray &
ADDRESSER: Borum
STREET: 6500 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/279,906A
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 5618922and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-279-906A-5

Query Match      36.6%; Score 26; DB 1; Length 8;
Best Local Similarity 80.0%; Pred. No. 3e+05; 1; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 1; Indels 0;

QY      6 HYRPG 10
      |||
      1 HIRPG 5

Db      1 HIRPG 5

RESULT 24
```

PCT-US92-06688-8
; Sequence 8, Application PC/TUS9206688
; GENERAL INFORMATION:
; APPLICANT: REPLICON CORPORATION
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MULTIPLE ANTIGEN PEPTIDES FOR USE AS HIV
; TITLE OF INVENTION: VACCINES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06688
; FILING DATE: 19920811
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 744,281
; FILING DATE: 13 August 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00231/052W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: AMINO ACID
; TOPOLOGY: linear
; PCT-US92-06688-8

Query Match 36.6%; Score 26; DB 5; Length 8;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 HYGPG 10
Db 3 HIGPG 7

RESULT 25
US-08-318-970B-23
; Sequence 23, Application US/08318970B
; Patent No. 5585573
; GENERAL INFORMATION:
; APPLICANT: HIDEAKI HAGIWARA, et al.
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF ANTI-IDIOTYPIC
; TITLE OF INVENTION: ANTIBODIES AGAINST ANTI-CANCER HUMAN MONOCLONAL ANTIBODY
; TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Law Office of Sherman and Shalloway
; STREET: 413 N. Washington Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: Dell System 210; Intel 80 285 Microprocessor
; OPERATING SYSTEM: MS DOS 3.3
; SOFTWARE: Word Perfect, Version 5.1

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,970B
; FILING DATE: October 6, 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard A. Steinberg
; REGISTRATION NUMBER: 26,588
; REFERENCE/DOCKET NUMBER: S-2371
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 549-2282
; TELEFAX: (703) 836-0106
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: L CDR3-5
; OTHER INFORMATION: hypervariable region.
US-08-318-970B-23

Query Match 36.6%; Score 26; DB 1; Length 9;
Best Local Similarity 42.9%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 KHYGPG 11
Db 2 QHYSTAW 8

RESULT 26
US-08-946-525-4
; Sequence 4, Application US/08946525
; Patent No. 6139843
; GENERAL INFORMATION:
; APPLICANT: AYE RUBINSTEIN, Barry R. Bloom, Yair Devash and Stanley J. Cryz
; TITLE OF INVENTION: PEPTIDE COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: PREVENTION OF HIV
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Amster, Rochstein & Ebenstein
; STREET: 90 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Processor (ASCII)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/946,525
; FILING DATE: October 7, 1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/785,696
; FILING DATE: January 17, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Bogosian, Elizabeth A
; REGISTRATION NUMBER: 39,911
; REFERENCE/DOCKET NUMBER: 96700/448
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-5995
; TELEFAX: (212) 286-0854 or 286-0082
; TELEX: TWX 710-581-4766
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear